

TABLE 3N

Genes Corresponding To Differentially Expressed Genes in Figure 21 - Depression					
Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4	0.025072	tetraspan 3 (TSPAN-3), mRNA /cds=(218,979) /gb=NM_005724 /gi=21264581 /ug=Hs.100090 /len=1842	NM_005724	Hs.100090	NP_005715
28	0.014741	602184410T1 NIH_MGC_42 cDNA clone IMAGE:4300347 3', mRNA sequence /clone=IMAGE:4300347 /clone_end=3' /gb=BF569051 /gi=11642431 /ug=Hs.352114 /len=1899	BF569051	Hs.352114	
33	0.024394	methionine adenosyltransferase II, alpha (MAT2A), mRNA /cds=(117,1304) /gb=NM_005911 /gi=19923346 /ug=Hs.77502 /len=2828	NM_005911	Hs.77502	NP_005902
42	0.025072	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (HADHA), mRNA /cds=(35,2326) /gb=NM_000182 /gi=20127407 /ug=Hs.75860 /len=2972	NM_000182	Hs.75860	NP_000173
98	0.020126	mitochondrion, complete genome	NC_001807		
104	0.034378	proteasome (prosome, macropain) activator subunit 2 (PA28 beta) (PSME2), mRNA /cds=(66,785) /gb=NM_002818 /gi=4506236 /ug=Hs.433810 /len=828	NM_002818	Hs.433810	NP_002809
154	0.034378	hypothetical protein DJ328E19.C1.1 (DJ328E19.C1.1), mRNA /cds=(18,2783) /gb=NM_015383 /gi=7657016 /ug=Hs.218329 /len=3689	NM_015383	Hs.218329	NP_056198
158	0.031002	CD36 antigen (collagen type I receptor, thrombospondin receptor) (CD36), mRNA /cds=(133,1551) /gb=NM_000072 /gi=4557418 /ug=Hs.75613 /len=1820	NM_000072	Hs.75613	NP_000063
171	0.006784	putative Rab5-interacting protein (RIP5), mRNA /cds=(183,572) /gb=NM_018840 /gi=10047115 /ug=Hs.184062 /len=1104	NM_018840	Hs.184062	NP_061328
178	0.01798	zinc finger protein 161 (ZNF161), mRNA /cds=(42,1592) /gb=NM_007146 /gi=6005967 /ug=Hs.223754 /len=2306	NM_007146	Hs.223754	NP_009077

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
209	0.006784	cyclin D2 (CCND2), mRNA /cds=(270,1139) /gb=NM_001759 /gi=16950656 /ug=Hs.75586 /len=6480	NM_001759	Hs.75586	NP_001750
210	0.020126	protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA /cds=(650,1171) /gb=NM_003463 /gi=17986281 /ug=Hs.227777 /len=4394	NM_003463	Hs.227777	NP_003454
224	0.031002	ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA /cds=(200,3508) /gb=NM_003470 /gi=4507856 /ug=Hs.78683 /len=4022	NM_003470	Hs.78683	NP_003461
225	0.020126	zinc finger protein 232 (ZNF232), mRNA /cds=(126,1379) /gb=NM_014519 /gi=7657704 /ug=Hs.279914 /len=1465	NM_014519	Hs.279914	NP_055334
251	0.011228	ATPase, Ca transporting, type 2C, member 1 (ATP2C1), mRNA /cds=(236,2995) /gb=NM_014382 /gi=7656909 /ug=Hs.106778 /len=3637	NM_014382	Hs.106778	NP_055197
255	0.031002	phenylalanyl-tRNA synthetase beta-subunit (FRSB), mRNA /cds=(14,1783) /gb=NM_005687 /gi=19923332 /ug=Hs.9081 /len=3118	NM_005687	Hs.9081	NP_005678
256	0.042048	KIAA0494 gene product (KIAA0494), mRNA /cds=(978,2465) /gb=NM_014774 /gi=7662159 /ug=Hs.62515 /len=5766	NM_014774	Hs.62515	NP_055589
259	0.020126	ornithine decarboxylase antizyme inhibitor (OAZIN), transcript variant 1, mRNA /cds=(721,2067) /gb=NM_015878 /gi=22538416 /ug=Hs.223014 /len=2882	NM_015878	Hs.223014	NP_680479
282	0.042048	protein phosphatase 1, regulatory (inhibitor) subunit 3C (PPP1R3C), mRNA /cds=(58,1011) /gb=NM_005398 /gi=21314622 /ug=Hs.303090 /len=2524	NM_005398	Hs.303090	NP_005389
283	0.020126	syntaxin 7 (STX7), mRNA /cds=(80,865) /gb=NM_003569 /gi=4507294 /ug=Hs.8906 /len=1614	NM_003569	Hs.8906	NP_003560
287	0.012669	zinc finger protein 187 (ZNF187), mRNA /cds=(193,1170) /gb=NM_152736 /gi=24211018 /ug=Hs.237786 /len=2298	NM_152736	Hs.237786	NP_689949

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
294	0.034378	mitochondrial carrier 2 (MTCH2), nuclear gene encoding mitochondrial protein, mRNA /cds=(49,960) /gb=NM_014342 /gi=7657346 /ug=Hs.279609 /len=1104	NM_014342	Hs.279609	NP_055157
310	0.022485	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
314	0.044138	601582740F1 NIH_MGC_7 cDNA clone IMAGE:3937377 5', mRNA sequence /clone=IMAGE:3937377 /clone_end=5' /gb=BE798080 /gi=10219278 /ug=Hs.446419 /len=1156	BE798080	Hs.446419	
332	0.022485	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
333	0.020126	chaperonin containing TCP1, subunit 8 (theta) (CCT8), mRNA /cds=(29,1675) /gb=NM_006585 /gi=6005726 /ug=Hs.15071 /len=1821	NM_006585	Hs.15071	NP_006576
357	0.022485	deleted in pancreatic carcinoma (DPC4) gene, exon 3	AF045440		
359	0.04638	plakophilin 2=X97675 plakophilin 2b (ORF 38%)	NP_004563		
361	0.032415	THO complex 1 (THOC1), mRNA /cds=(15,1988) /gb=NM_005131 /gi=4826881 /ug=Hs.1540 /len=2092	NM_005131	Hs.1540	NP_005122
366	0.042048	voltage-dependent anion channel 1 (VDAC1), mRNA /cds=(100,951) /gb=NM_003374 /gi=4507878 /ug=Hs.149155 /len=1806	NM_003374	Hs.149155	NP_003365
370	0.04638	carboxypeptidase E (CPE), mRNA /cds=(291,1721) /gb=NM_001873 /gi=4503008 /ug=Hs.75360 /len=2443	NM_001873	Hs.75360	NP_001864
372	0.009931	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26 (DDX26), mRNA /cds=(477,3140) /gb=NM_012141 /gi=11024693 /ug=Hs.58570 /len=3690	NM_012141	Hs.58570	NP_036273
380	0.031002	5'-3' exoribonuclease 2 (XRN2), mRNA /cds=(86,2938) /gb=NM_012255 /gi=18860915 /ug=Hs.268555 /len=3445	NM_012255	Hs.268555	NP_036387

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
384	0.031002	ADP-ribosylation factor-like 6 interacting protein (ARL6IP), mRNA /cds=(70,681) /gb=NM_015161 /gi=24308006 /ug=Hs.75249 /len=2280	NM_015161	Hs.75249	NP_055976
385	0.042048	cyclin C (CCNC), mRNA /cds=(29,940) /gb=NM_005190 /gi=7382485 /ug=Hs.118442 /len=1508	NM_005190	Hs.118442	NP_005181
390	0.038054	UDP-galactose transporter related (UGTREL1), mRNA /cds=(88,1056) /gb=NM_005827 /gi=5032212 /ug=Hs.154073 /len=1186	NM_005827	Hs.154073	NP_005818
393	0.020126	microsomal epoxide hydrolase (EPHX1) gene, complete cds	AF253417		
395	0.014265	cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1), mRNA /cds=(85,1083) /gb=NM_012124 /gi=6912303 /ug=Hs.22857 /len=2058	NM_012124	Hs.22857	NP_036256
396	0.04638	hypothetical protein FLJ20445 (FLJ20445), mRNA /cds=(293,1129) /gb=NM_017824 /gi=19923500 /ug=Hs.343748 /len=3896	NM_017824	Hs.343748	NP_060294
409	0.008765	S-phase kinase-associated protein 1A (p19A) (SKP1A), transcript variant 1, mRNA /cds=(140,622) /gb=NM_006930 /gi=25777710 /ug=Hs.171626 /len=2172	NM_006930	Hs.171626	NP_733779
417	0.027906	LATS, large tumor suppressor, 2 (Drosophila) (LATS2), mRNA /cds=(375,3641) /gb=NM_014572 /gi=18959199 /ug=Hs.432314 /len=4098	NM_014572	Hs.432314	NP_055387
427	0.04638	hypothetical protein FLJ20508 (FLJ20508), mRNA /cds=(191,802) /gb=NM_017850 /gi=8923468 /ug=Hs.272673 /len=2376	NM_017850	Hs.272673	NP_060320
429	0.008765	NPD009 protein (NPD009), mRNA /cds=(1327,1677) /gb=NM_020686 /gi=24476005 /ug=Hs.283675 /len=2514	NM_020686	Hs.283675	NP_065737
432	0.042048	DKFZp586L081 (from clone DKFZp586L081) /cds=UNKNOWN /gb=AL080234 /gi=5262727 /ug=Hs.8078 /len=2159	AL080234	Hs.8078	
439	0.006784	COBW domain-containing protein mRNA, complete cds /cds=(35,1222) /gb=AF452722 /gi=24850425 /ug=Hs.434050 /len=1561	AF452722	Hs.434050	

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
459	0.012669	X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), transcript variant 3, mRNA /cds=(176,1180) /gb=NM_022550 /gi=12408648 /ug=Hs.150930 /len=1707	NM_022550	Hs.150930	NP_072044
461	0.009931	a disintegrin-like and metalloprotease (repolysin type) with thrombospondin type 1 motif, 1 (ADAMTS1), mRNA /cds=(294,3146) /gb=NM_006988 /gi=11038653 /ug=Hs.8230 /len=4459	NM_006988	Hs.8230	NP_008919
462	0.027906	erg protein (ets-related gene)	M21535		NP_004440
466	0.00772	activity-dependent neuroprotector (ADNP), mRNA /cds=(346,3654) /gb=NM_015339 /gi=12229216 /ug=Hs.3657 /len=4713	NM_015339	Hs.3657	NP_056154
512	0.027906	myosin IXB (MYO9B), mRNA /cds=(1,6069) /gb=NM_004145 /gi=4758749 /ug=Hs.159629 /len=6069	NM_004145	Hs.159629	NP_004136
517	0.015802	galactokinase 1 (GALK1), mRNA /cds=(64,1242) /gb=NM_000154 /gi=4503894 /ug=Hs.92357 /len=1361	NM_000154	Hs.92357	NP_000145
518	0.02729	small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen) (SNRP70), mRNA /cds=(681,2525) /gb=NM_003089 /gi=4507118 /ug=Hs.174051 /len=2693	NM_003089	Hs.174051	NP_003080
573	0.034378	ancient ubiquitous protein 1 (AUP1), mRNA /cds=(69,1499) /gb=NM_012103 /gi=6912259 /ug=Hs.173736 /len=1664	NM_012103	Hs.173736	NP_036235
574	0.013065	mRNA for KIAA1274 protein, partial cds. /cds=(265,2850) /gb=AB033100 /gi=20521819 /ug=Hs.300646 /len=4569	AB033100	Hs.300646	
605	0.044138	integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5), mRNA /cds=(24,3173) /gb=NM_002205 /gi=4504750 /ug=Hs.149609 /len=4204	NM_002205	Hs.149609	NP_002196
612	0.022485	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 (FAU), mRNA /cds=(106,507) /gb=NM_001997 /gi=17981709 /ug=Hs.177415 /len=574	NM_001997	Hs.177415	NP_001988

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
615	0.020126	cDNA FLJ11904 fis, clone HEMBB1000048. /gb=AK021966 /gi=10433275 /ug=Hs.285519 /len=2134	AK021966	Hs.285519	
633	0.022485	A kinase (PRKA) anchor protein 13 (AKAP13), transcript variant 2, mRNA /cds=(214,8655) /gb=NM_007200 /gi=21493028 /ug=Hs.301946 /len=10156	NM_007200	Hs.301946	NP_658913
645	0.042048	hematopoietic-derived zinc fingerprotein (RefSeq aa 1e-48)	NP_004867		
672	0.035996	C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA /cds=(137,3094) /gb=NM_022802 /gi=12746589 /ug=Hs.171391 /len=3780	NM_022802	Hs.171391	NP_073713
726	0.031002	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide (YWHAG), mRNA /cds=(192,935) /gb=NM_012479 /gi=21464100 /ug=Hs.25001 /len=3747	NM_012479	Hs.25001	NP_036611
749	0.034378	ribosomal protein S24 (RPS24), transcript variant 1, mRNA /cds=(38,430) /gb=NM_033022 /gi=14916500 /ug=Hs.180450 /len=537	NM_033022	Hs.180450	NP_148982
779	0.012669	myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA /cds=(1,5883) /gb=NM_002473 /gi=22507396 /ug=Hs.146550 /len=7274	NM_002473	Hs.146550	NP_002464
802	0.025072	striated muscle contraction regulatory protein (Id2B) mRNA, complete cds. /cds=(110,220) /gb=M96843 /gi=397775 /ug=Hs.296811 /len=1167	M96843	Hs.296811	
808	0.022485	PIX1 mRNA (ORF)	AF037219		NP_570854
809	0.020912	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) (MCCC1), mRNA /cds=(133,2310) /gb=NM_020166 /gi=13518227 /ug=Hs.47649 /len=2528	NM_020166	Hs.47649	NP_064551
833	0.042048	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa (NDUFB3), mRNA /cds=(253,549) /gb=NM_002491 /gi=4505360 /ug=Hs.109760 /len=693	NM_002491	Hs.109760	NP_002482

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
842	0.031002	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E (SEMA3E), mRNA /cds=(467,2794) /gb=NM_012431 /gi=6912649 /ug=Hs.212414 /len=6474	NM_012431	Hs.212414	NP_036563
851	0.027906	of89c05.s1 NCI_CGAP_Li5 cDNA clone IMAGE:1437512 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:1437512 /clone_end=3' /gb=AA894384 /gi=3030785 /ug=Hs.432123 /len=296	AA894384	Hs.432123	
877	0.027906	ring finger protein 11 (RNF11), mRNA /cds=(128,592) /gb=NM_014372 /gi=7657519 /ug=Hs.96334 /len=2529	NM_014372	Hs.96334	NP_055187
885	0.031002	mRNA for KIAA1350 protein, partial cds. /cds=(1,2737) /gb=AB037771 /gi=7243080 /ug=Hs.101799 /len=4153	AB037771	Hs.101799	
900	0.042048	RAB11A, member RAS oncogene family (RAB11A), mRNA /cds=(104,754) /gb=NM_004663 /gi=20149549 /ug=Hs.75618 /len=2474	NM_004663	Hs.75618	NP_004654
902	0.01798	H2A histone family, member Z (H2AFZ), mRNA /cds=(107,493) /gb=NM_002106 /gi=20336749 /ug=Hs.119192 /len=873	NM_002106	Hs.119192	NP_002097
903	0.038054	S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA /cds=(112,405) /gb=NM_002966 /gi=4506760 /ug=Hs.400250 /len=649	NM_002966	Hs.400250	NP_002957
918	0.022485	AGENCOURT_6456859 NIH_MGC_92 cDNA clone IMAGE:5576908 5', mRNA sequence /clone=IMAGE:5576908 /clone_end=5' /gb=BM466169 /gi=18515211 /ug=Hs.439148 /len=1150	BM466169	Hs.439148	
925	0.00772	OGT(O-Glc-NAc transferase)-interacting protein 106 KDa (OIP106), mRNA /cds=(217,3078) /gb=NM_014965 /gi=7662457 /ug=Hs.6705 /len=5109	NM_014965	Hs.6705	NP_055780
941	0.038054	polybromo 1 (PB1), mRNA /cds=(15,935) /gb=NM_018165 /gi=8922564 /ug=Hs.44143 /len=3131	NM_018165	Hs.44143	NP_060783

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Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
952	0.01798	mRNA; cDNA DKFZp451O194 (from clone DKFZp451O194) /gb=AL832029 /gi=21732569 /ug=Hs.22559 /len=5226	AL832029	Hs.22559	
953	0.04638	mRNA for KIAA0592 protein, partial cds. /cds=(1,4062) /gb=AB011164 /gi=3043707 /ug=Hs.439367 /len=4623	AB011164	Hs.439367	
961	0.042048	SON DNA binding protein (SON), transcript variant e, mRNA /cds=(50,6376) /gb=NM_058183 /gi=21040317 /ug=Hs.92909 /len=8482	NM_058183	Hs.92909	NP_620305
966	0.031002	CGI-81 protein (DREV1), mRNA /cds=(249,1100) /gb=NM_016025 /gi=19923448 /ug=Hs.279583 /len=3163	NM_016025	Hs.279583	NP_057109
973	0.02015	heat shock factor binding protein 1 (HSBP1), mRNA /cds=(55,285) /gb=NM_001537 /gi=4557646 /ug=Hs.250899 /len=547	NM_001537	Hs.250899	NP_001528
987	0.038054	brain protein 44-like (BRP44L), mRNA /cds=(123,452) /gb=NM_016098 /gi=7706368 /ug=Hs.108725 /len=988	NM_016098	Hs.108725	NP_057182
995	0.034378	homeodomain-interacting protein kinase 3 (HIPK3), mRNA /cds=(5,3652) /gb=NM_005734 /gi=11386208 /ug=Hs.30148 /len=3723	NM_005734	Hs.30148	NP_005725
1040	0.042048	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa (NDUFB2), mRNA /cds=(58,375) /gb=NM_004546 /gi=4758777 /ug=Hs.198272 /len=494	NM_004546	Hs.198272	NP_004537
1043	0.038054	mRNA for KIAA1376 protein, partial cds. /cds=(144,1457) /gb=AB037797 /gi=7243132 /ug=Hs.24684 /len=4131	AB037797	Hs.24684	
1044	0.005949	par-3 partitioning defective 3 (C. elegans) (PAR3), mRNA /cds=(1,4071) /gb=NM_019619 /gi=21361830 /ug=Hs.72249 /len=4071	NM_019619	Hs.72249	NP_062565
1062	0.04638	filamin B, beta (actin binding protein 278) (FLNB), mRNA /cds=(132,7940) /gb=NM_001457 /gi=4503746 /ug=Hs.81008 /len=9432	NM_001457	Hs.81008	NP_001448



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1065	0.027906	cytochrome c oxidase subunit VIa polypeptide 2 (COX6A2), nuclear gene encoding mitochondrial protein, mRNA /cds=(76,369) /gb=NM_005205 /gi=17999529 /ug=Hs.250760 /len=425	NM_005205	Hs.250760	NP_005196
1066	0.038054	hypothetical protein FLJ20452 (FLJ20452), mRNA /cds=(15,614) /gb=NM_017828 /gi=21361660 /ug=Hs.351327 /len=1948	NM_017828	Hs.351327	NP_060298
1068	0.025072	UPF3 regulator of nonsense transcripts A (yeast) (UPF3A), transcript variant 1, mRNA /cds=(38,1468) /gb=NM_023011 /gi=18375523 /ug=Hs.399740 /len=2381	NM_023011	Hs.399740	NP_542418
1084	0.034378	ADP-ribosylation factor-like 1 (ARL1), mRNA /cds=(105,650) /gb=NM_001177 /gi=4755126 /ug=Hs.242894 /len=968	NM_001177	Hs.242894	NP_001168
1090	0.031002	protein phosphatase methylesterase-1 (PME-1), mRNA /cds=(100,1260) /gb=NM_016147 /gi=7706644 /ug=Hs.63304 /len=2484	NM_016147	Hs.63304	NP_057231
1148	0.034378	CHLORIDE INTRACELLULAR CHANNEL PROTEIN 1 (NUCLEAR CHLORIDE ION CHANNEL 27) (NCC27) (P64 CLCP) (aa 2e-14 92%)	Q9Z1Q5		
1149	0.012669	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1), transcript variant 7, mRNA /cds=(727,2715) /gb=NM_023109 /gi=13186244 /ug=Hs.748 /len=4066	NM_023109	Hs.748	NP_075599
1164	0.034378	suppressor of Ty 5 (S. cerevisiae) (SUPT5H), mRNA /cds=(208,3471) /gb=NM_003169 /gi=20149523 /ug=Hs.70186 /len=3762	NM_003169	Hs.70186	NP_003160
1171	0.025072	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12) (ITGB1), transcript variant 1A, mRNA /cds=(127,2523) /gb=NM_002211 /gi=19743812 /ug=Hs.287797 /len=3700	NM_002211	Hs.287797	NP_596867
1180	0.006784	complement component 2 (C2), mRNA /cds=(37,2295) /gb=NM_000063 /gi=20631970 /ug=Hs.2253 /len=2609	NM_000063	Hs.2253	NP_000054

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1184	0.009931	mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA /cds=(521,2446) /gb=NM_006699 /gi=5729912 /ug=Hs.367638 /len=2792	NM_006699	Hs.367638	NP_006690
1185	0.027906	novel protein AHNAK mRNA, partial sequence. /cds=(1,3836) /gb=M80899 /gi=178282 /ug=Hs.381240 /len=4051	M80899	Hs.381240	
1186	0.031002	ankylosis, progressive (mouse) (ANKH), transcript variant 2, mRNA /cds=(265,1743) /gb=NM_054027 /gi=21536394 /ug=Hs.168640 /len=4031	NM_054027	Hs.168640	NP_473368
1200	0.014265	hypothetical gene supported by XM_000590 (LOC59176)	XM_000590		
1201	0.034378	DKFZp564D177 protein (DKFZp564D177), mRNA /cds=(106,849) /gb=NM_015469 /gi=22267435 /ug=Hs.24608 /len=1664	NM_015469	Hs.24608	NP_056284
1206	0.042048	ATP synthase, H transporting, mitochondrial F1 complex, gamma polypeptide 1 (ATP5C1), mRNA /cds=(32,925) /gb=NM_005174 /gi=4885078 /ug=Hs.155433 /len=1078	NM_005174	Hs.155433	NP_005165
1210	0.025072	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase) (NDUFS1), mRNA /cds=(85,2268) /gb=NM_005006 /gi=28269700 /ug=Hs.8248 /len=2382	NM_005006	Hs.8248	NP_004997
1213	0.04638	heat shock 10kDa protein 1 (chaperonin 10) (HSP1), mRNA /cds=(42,350) /gb=NM_002157 /gi=4504522 /ug=Hs.1197 /len=538	NM_002157	Hs.1197	NP_002148
1214	0.005206	mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4254	AL080209	Hs.13659	
1217	0.016031	DKFZp586F1918 (from clone DKFZp586F1918); partial cds	AL050091		NP_056347
1220	0.008765	mRNA; cDNA DKFZp547C244 (from clone DKFZp547C244) /gb=AL442093 /gi=10241768 /ug=Hs.9460 /len=2537	AL442093	Hs.9460	
1227	0.020126	integral inner nuclear membrane protein (MAN1), mRNA /cds=(7,2742) /gb=NM_014319 /gi=7706606 /ug=Hs.7256 /len=4703	NM_014319	Hs.7256	NP_055134

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1238	0.031002	mRNA for KIAA1673 protein, partial cds. /cds=(69,2207) /gb=AB051460 /gi=12697890 /ug=Hs.301444 /len=6380	AB051460	Hs.301444	
1242	0.014265	programmed cell death 4 (neoplastic transformation inhibitor) (PDCD4), transcript variant 2, mRNA /cds=(361,1737) /gb=NM_145341 /gi=21735597 /ug=Hs.326248 /len=2403	NM_145341	Hs.326248	NP_663314
1250	0.005206	nuclear protein, ataxia-telangiectasia locus (NPAT), mRNA /cds=(35,4318) /gb=NM_002519 /gi=4505430 /ug=Hs.89385 /len=5895	NM_002519	Hs.89385	NP_002510
1255	0.014265	protein inhibitor of activated STAT, 1 (PIAS1), mRNA /cds=(97,2052) /gb=NM_016166 /gi=7706636 /ug=Hs.75251 /len=2309	NM_016166	Hs.75251	NP_057250
1261	0.010197	cDNA FLJ11971 fis, clone HEMBB1001208. /gb=AK022033 /gi=10433350 /ug=Hs.121806 /len=2355	AK022033	Hs.121806	
1281	0.020912	tripartite motif-containing 44 (TRIM44), mRNA /cds=(217,1251) /gb=NM_017583 /gi=21361638 /ug=Hs.14512 /len=3091	NM_017583	Hs.14512	NP_060053
1306	0.039896	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182	NP_002559
1309	0.04638	oxysterol binding protein-like 11 (OSBPL11), mRNA /cds=(306,2549) /gb=NM_022776 /gi=23111058 /ug=Hs.61260 /len=4206	NM_022776	Hs.61260	NP_073613
1335	0.013065	hypothetical protein MGC11316 (MGC11316), mRNA /cds=(116,226) /gb=NM_032932 /gi=14249729 /ug=Hs.7985 /len=781	NM_032932	Hs.7985	NP_116321
1336	0.04638	Novel mRNA from chromosome 1, which has similarities to BAT2 genes /cds=(58,8163) /gb=AL096857 /gi=5541862 /ug=Hs.69559 /len=10174	AL096857	Hs.69559	NP_055987
1338	0.014265	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent phospholipase A2) (AOP2), mRNA /cds=(44,718) /gb=NM_004905 /gi=4758637 /ug=Hs.120 /len=1653	NM_004905	Hs.120	NP_004896

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1339	0.031002	FLJ20398 fis, clone KAT00580, highly similar to M35604 Human glucose-6-phosphate dehydrogenase /cds=UNKNOWN /gb=AK000405 /gi=7020471 /ug=Hs.76480 /len=2342 (=FLN, =G6PD, =ubiquitin-like protein (GdX))	AK000405	Hs.76480	NP_055050
1342	0.04638	FLJ30731 fis, clone FEBRA2000105, moderately similar to KINESIN LIGHT CHAIN /cds=UNKNOWN /gb=AK055293 /gi=16549995 /ug=Hs.53447 /len=2770	AK055293	Hs.53447	NP_612352
1345	0.04638	WW domain binding protein 1 (WBP1), mRNA /cds=(154,963) /gb=NM_012477 /gi=24430130 /ug=Hs.7709 /len=1183	NM_012477	Hs.7709	NP_036609
1355	0.032415	FLJ13418 fis, clone PLACE1002090, highly similar to SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (AK023480.1)	AK023480	Hs.237825	NP_008878
1358	0.034378	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
1360	0.005206	chromosome 15 open reading frame 15 (C15orf15), mRNA /cds=(144,635) /gb=NM_016304 /gi=18491027 /ug=Hs.284162 /len=1487	NM_016304	Hs.284162	NP_057388
1362	0.01798	ADP-ribosylation factor related protein 1 (ARFRP1), mRNA /cds=(12,617) /gb=NM_003224 /gi=4507448 /ug=Hs.389277 /len=1559	NM_003224	Hs.389277	NP_003215
1366	0.016031	Rho guanine nucleotide exchange factor (GEF) 3 (ARHGEF3), mRNA /cds=(128,1708) /gb=NM_019555 /gi=9506400 /ug=Hs.25951 /len=3561	NM_019555	Hs.25951	NP_062455
1373	0.016031	hypothetical protein MGC14421 (MGC14421), mRNA /cds=(474,1616) /gb=NM_032907 /gi=14249681 /ug=Hs.334713 /len=1772	NM_032907	Hs.334713	NP_116296
1376	0.008765	chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA /cds=(92,1717) /gb=NM_012073 /gi=24307938 /ug=Hs.1600 /len=1961	NM_012073	Hs.1600	NP_036205
1386	0.020912	AGENCOURT_6424254 NIH_MGC_67 cDNA clone IMAGE:5491531 5', mRNA sequence /clone=IMAGE:5491531 /clone_end=5' /gb=BM479954 /gi=18528996 /ug=Hs.381243 /len=1112	BM479954	Hs.381243	

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1396	0.01798	enoyl Coenzyme A hydratase 1, peroxisomal (ECH1), mRNA /cds=(28,1014) /gb=NM_001398 /gi=4503446 /ug=Hs.196176 /len=1196	NM_001398	Hs.196176	NP_001389
1403	0.014265	potassium voltage-gated channel, KQT-like subfamily, member 2 (KCNQ2), transcript variant 3, mRNA /cds=(178,2712) /gb=NM_004518 /gi=26051259 /ug=Hs.4975 /len=7556	NM_004518	Hs.4975	NP_742107
1413	0.031002	vacuolar protein sorting 29 (yeast) (VPS29) transcript variant 2, mRNA /cds=(61,621) /gb=NM_057180 /gi=17402911 /ug=Hs.69192 /len=1107	NM_057180	Hs.69192	NP_476528
1419	0.027906	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA /cds=(8,706) /gb=NM_004355 /gi=10835070 /ug=Hs.84298 /len=1304	NM_004355	Hs.84298	NP_004346
1503	0.04638	retrovirus-related leucine zipper protein p40 - human retrotransposon L1.1	I38587		
1540	0.025072	ribosomal protein S4, X-linked (RPS4X), mRNA /cds=(36,827) /gb=NM_001007 /gi=17981705 /ug=Hs.389933 /len=916	NM_001007	Hs.389933	NP_000998
1557	0.034378	MR2-CI0186-291100-010-a06 CI0186 cDNA, mRNA sequence /gb=BF814502 /gi=12147047 /ug=Hs.446594 /len=530	BF814502	Hs.446594	
1559	0.025072	stromal cell derived factor receptor 1 (SDFR1), transcript variant beta, mRNA /cds=(139,1335) /gb=NM_012428 /gi=6912645 /ug=Hs.389371 /len=2388	NM_012428	Hs.389371	NP_059429
1564	0.027906	quiescin Q6 (QSCN6), mRNA /cds=(76,2319) /gb=NM_002826 /gi=13325074 /ug=Hs.77266 /len=3314	NM_002826	Hs.77266	NP_002817
1579	0.031002	chromosome 14 open reading frame 108 (C14orf108), mRNA /cds=(407,1879) /gb=NM_018229 /gi=21361775 /ug=Hs.106210 /len=3088	NM_018229	Hs.106210	NP_060699
1586	0.020126	KIAA1665 protein, partial cds /cds=UNKNOWN /gb=AB051452 /gi=13359202 /ug=Hs.300463 /len=4311	AB051452	Hs.300463	NP_612211

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1596	0.042048	mRNA for KIAA1824 protein, partial cds. /cds=(7,2883) /gb=AB058727 /gi=14017864 /ug=Hs.284294 /len=5814	AB058727	Hs.284294	
1597	0.006784	ATPase, H transporting, lysosomal 16kDa, V0 subunit c (ATP6V0C), mRNA /cds=(153,620) /gb=NM_001694 /gi=19913436 /ug=Hs.389107 /len=1126	NM_001694	Hs.389107	NP_001685
1621	0.034378	mRNA for KIAA1856 protein, partial cds. /cds=(1,3405) /gb=AB058759 /gi=14017928 /ug=Hs.381163 /len=5223	AB058759	Hs.381163	
1637	0.034378	ribosomal protein S16 (RPS16), mRNA /cds=(53,493) /gb=NM_001020 /gi=14591912 /ug=Hs.397609 /len=570	NM_001020	Hs.397609	NP_001011
1667	0.009931	interleukin 1 receptor, type I (IL1R1), mRNA /cds=(83,1792) /gb=NM_000877 /gi=27894331 /ug=Hs.82112 /len=4909	NM_000877	Hs.82112	NP_000868
1684	0.01798	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
1685	0.042048	hypothetical protein FLJ20059 (FLJ20059), mRNA /cds=(26,1291) /gb=NM_017644 /gi=8923060 /ug=Hs.246875 /len=1817	NM_017644	Hs.246875	NP_060114
1699	0.014265	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 3 (SLC11A3), mRNA /cds=(315,2030) /gb=NM_014585 /gi=19923794 /ug=Hs.5944 /len=3333	NM_014585	Hs.5944	NP_055400
1753	0.027906	phosphorylase kinase, beta (PHKB), mRNA /cds=(25,3306) /gb=NM_000293 /gi=4505782 /ug=Hs.78060 /len=4284	NM_000293	Hs.78060	NP_000284
1806	0.027906	hypothetical protein FLJ10134 (FLJ10134), mRNA /cds=(314,1141) /gb=NM_018004 /gi=8922242 /ug=Hs.104800 /len=1564	NM_018004	Hs.104800	NP_060474
1817	0.04638	mRNA; cDNA DKFZp761P18121 (from clone DKFZp761P18121) /cds=(127,2289) /gb=AL834147 /gi=21739620 /ug=Hs.44198 /len=4286	AL834147	Hs.44198	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
1831	0.038054	mRNA; cDNA DKFZp686O1729 (from clone DKFZp686O1729) /gb=AL833498 /gi=21734141 /ug=Hs.109731 /len=2003	AL833498	Hs.109731	
1834	0.014265	cDNA FLJ14337 fis, clone PLACE4000494. /gb=AK024399 /gi=10436778 /ug=Hs.180187 /len=4588	AK024399	Hs.180187	
1866	0.042048	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta) (PPP3CB), mRNA /cds=(117,1691) /gb=NM_021132 /gi=11036639 /ug=Hs.151531 /len=3079	NM_021132	Hs.151531	NP_066955
1889	0.027906	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide (YWHAH), mRNA /cds=(198,938) /gb=NM_003405 /gi=21464102 /ug=Hs.349530 /len=1775	NM_003405	Hs.349530	NP_003396
1933	0.016031	mRNA for KIAA0361 gene, KIAA0361 protein. /cds=(1,4117) /gb=AB002359 /gi=2224662 /ug=Hs.105478 /len=5338	AB002359	Hs.105478	
1973	0.00344	keratin 8 (KRT8), mRNA /cds=(60,1511) /gb=NM_002273 /gi=4504918 /ug=Hs.242463 /len=1752	NM_002273	Hs.242463	NP_002264
1999	0.011228	chromosome 20 open reading frame 40 (C20orf40), mRNA /cds=(208,396) /gb=NM_014054 /gi=7661709 /ug=Hs.105379 /len=417	NM_014054	Hs.105379	NP_054773
2001	0.042048	mRNA for KIAA0892 protein, partial cds. /cds=(1,1867) /gb=AB020699 /gi=4240272 /ug=Hs.112751 /len=4164	AB020699	Hs.112751	
2002	0.034378	ANG2 (ANG2)	AF024631		NP_008917
2006	0.034378	clathrin, light polypeptide (Lcb) (CLTB), transcript variant brain, mRNA /cds=(173,862) /gb=NM_007097 /gi=6005994 /ug=Hs.380749 /len=1134	NM_007097	Hs.380749	NP_009028
2042	0.016031	ARF protein (LOC51326), mRNA /cds=(88,489) /gb=NM_016632 /gi=7706177 /ug=Hs.264509 /len=826	NM_016632	Hs.264509	NP_057716
2095	0.012669	chromosome 19 open reading frame 2 (C19orf2), transcript variant 1, mRNA /cds=(31,1638) /gb=NM_003796 /gi=19924158 /ug=Hs.7943 /len=2295	NM_003796	Hs.7943	NP_604431

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2107	0.014265	HSPC126 protein (HSPC126), mRNA /cds=(26,838) /gb=NM_014166 /gi=7661787 /ug=Hs.181112 /len=1424	NM_014166	Hs.181112	NP_054885
2112	0.005206	NRH:quinone oxidoreductase 2 gene (NQO2)	AB050248		
2143	0.012669	chromosome 13 open reading frame 9 (C13orf9), mRNA /cds=(6,1166) /gb=NM_016075 /gi=7705639 /ug=Hs.146324 /len=1832	NM_016075	Hs.146324	NP_057159
2160	0.016031	mannosidase, alpha, class 1A, member 2 (MAN1A2), mRNA /cds=(521,2446) /gb=NM_006699 /gi=5729912 /ug=Hs.367638 /len=2792	NM_006699	Hs.367638	NP_006690
2167	0.034378	copine III (CPNE3), mRNA /cds=(121,1734) /gb=NM_003909 /gi=4503014 /ug=Hs.14158 /len=4737	NM_003909	Hs.14158	NP_003900
2176	0.027906	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12), mRNA /cds=(44,1414) /gb=NM_002816 /gi=4506220 /ug=Hs.4295 /len=3548	NM_002816	Hs.4295	NP_777360
2177	0.042048	RAB34, member RAS oncogene family (RAB34), mRNA /cds=(206,985) /gb=NM_031934 /gi=21361998 /ug=Hs.301853 /len=1340	NM_031934	Hs.301853	NP_114140
2178	0.031002	crystallin, zeta (quinone reductase)-like 1 (CRYZL1), transcript variant 3, mRNA /cds=(86,682) /gb=NM_145858 /gi=22202615 /ug=Hs.330208 /len=2099	NM_145858	Hs.330208	NP_665857
2184	0.031002	highly charged protein (D13S106E), mRNA /cds=(178,3456) /gb=NM_005800 /gi=5031648 /ug=Hs.151236 /len=3650	NM_005800	Hs.151236	NP_005791
2207	0.027906	nidogen 2 (osteonidogen) (NID2), mRNA /cds=(1,4131) /gb=NM_007361 /gi=6679055 /ug=Hs.82733 /len=4829	NM_007361	Hs.82733	NP_031387
2217	0.027906	nebulette (NEBL), mRNA /cds=(398,3442) /gb=NM_006393 /gi=5453757 /ug=Hs.5025 /len=8034	NM_006393	Hs.5025	NP_006384
2221	0.038054	clone MGC:43950 IMAGE:5276217, mRNA, complete cds /cds=(351,392) /gb=BC037901 /gi=23138800 /ug=Hs.262716 /len=2214	BC037901	Hs.262716	
2239	0.020126	hypothetical protein (KIAA1162)	AB032988		NP_066979



**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2244	0.022485	F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 2, mRNA /cds=(586,2283) /gb=NM_033535 /gi=21536439 /ug=Hs.5548 /len=3475	NM_033535	Hs.5548	NP_277077
2288	0.008765	Similar to hypothetical protein MGC30540, clone MGC:17342 IMAGE:4342258, mRNA, complete cds /cds=(216,1457) /gb=BC042899 /gi=27552863 /ug=Hs.153716 /len=3028	BC042899	Hs.153716	NP_671512
2310	0.020126	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA /cds=(503,2404) /gb=NM_002568 /gi=4505574 /ug=Hs.172182 /len=2848	NM_002568	Hs.172182	NP_002559
2311	0.008765	thyroid hormone receptor-associated protein, 150 kDa subunit (TRAP150), mRNA /cds=(203,3070) /gb=NM_005119 /gi=4827039 /ug=Hs.108319 /len=3618	NM_005119	Hs.108319	NP_005110
2330	0.034374	eukaryotic translation elongation factor 2 (EEF2), mRNA /cds=(69,2645) /gb=NM_001961 /gi=25453476 /ug=Hs.75309 /len=3148	NM_001961	Hs.75309	NP_001952
2358	0.016031	cDNA FLJ90297 fis, clone NT2RP2000447, moderately similar to GOLGIN-95. /cds=(333,728) /gb=AK074778 /gi=22760446 /ug=Hs.405809 /len=2520	AK074778	Hs.405809	
2360	0.038054	hepatocyte growth factor-like protein homolog (low match)	U28055		
2368	0.020126	capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA /cds=(1,819) /gb=NM_004930 /gi=4826658 /ug=Hs.333417 /len=1077	NM_004930	Hs.333417	NP_004921
2413	0.031002	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3), mRNA /cds=(165,1769) /gb=NM_002809 /gi=25777611 /ug=Hs.9736 /len=2174	NM_002809	Hs.9736	NP_002800
2435	0.01798	ribosome binding protein 1 180kDa (dog) (RRBP1), mRNA /cds=(71,3004) /gb=NM_004587 /gi=4759055 /ug=Hs.98614 /len=3106	NM_004587	Hs.98614	NP_004578
2446	0.008765	oxysterol binding protein-like 2 (OSBPL2), transcript variant 2, mRNA /cds=(203,1645) /gb=NM_144498 /gi=21450852 /ug=Hs.15519 /len=3971	NM_144498	Hs.15519	NP_653081

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2461	0.014265	annexin A6 (ANXA6), transcript variant 1, mRNA /cds=(171,2192) /gb=NM_001155 /gi=4809274 /ug=Hs.118796 /len=2528	NM_001155	Hs.118796	NP_004024
2476	0.022485	MAP kinase-interacting serine/threonine kinase 1 (MKNK1), mRNA /cds=(174,1571) /gb=NM_003684 /gi=21361100 /ug=Hs.5591 /len=2745	NM_003684	Hs.5591	NP_003675
2477	0.025072	of human GTP-binding protein G25K	AL121737		NP_426359
2488	0.025072	likely ortholog of mouse hippocampus abundant gene transcript 1 (HIAT1), mRNA /cds=(6,1124) /gb=NM_033055 /gi=24308343 /ug=Hs.21015 /len=2230	NM_033055	Hs.21015	NP_149044
2508	0.034378	sorting nexin 1 (SNX1), transcript variant 1, mRNA /cds=(13,1581) /gb=NM_003099 /gi=23111033 /ug=Hs.75283 /len=1984	NM_003099	Hs.75283	NP_690039
2520	0.002982	KIAA0164 gene product (KIAA0164), mRNA /cds=(254,3016) /gb=NM_014739 /gi=7661957 /ug=Hs.80338 /len=5538	NM_014739	Hs.80338	NP_055554
2533	0.016031	kinase substrate HASPP28 mRNA, complete cds	U26541		
2545	0.031002	chromosome 8 open reading frame 1 (C8orf1), mRNA /cds=(346,1863) /gb=NM_004337 /gi=4757889 /ug=Hs.40539 /len=4199	NM_004337	Hs.40539	NP_004328
2546	0.01798	vascular endothelial growth factor (VEGF), mRNA /cds=(702,1277) /gb=NM_003376 /gi=19923239 /ug=Hs.73793 /len=3166	NM_003376	Hs.73793	NP_003367
2547	0.031002	B-cell CLL/lymphoma 3 (BCL3), mRNA /cds=(42,1382) /gb=NM_005178 /gi=20336471 /ug=Hs.31210 /len=1813	NM_005178	Hs.31210	NP_005169
2553	0.027906	transmembrane protein vezatin (VEZATIN), mRNA /cds=(177,1886) /gb=NM_017599 /gi=19923537 /ug=Hs.24135 /len=3949	NM_017599	Hs.24135	NP_060069
2568	0.011228	glycoprotein M6B (GPM6B), mRNA /cds=(255,1052) /gb=NM_005278 /gi=24307894 /ug=Hs.5422 /len=1642	NM_005278	Hs.5422	NP_005269
2569	0.038054	PEST-containing nuclear protein (PCNP), mRNA /cds=(19,555) /gb=NM_020357 /gi=9966826 /ug=Hs.71618 /len=2250	NM_020357	Hs.71618	NP_065090

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2583	0.014265	receptor (calcitonin) activity modifying protein 3 (RAMP3), mRNA /cds=(30,476) /gb=NM_005856 /gi=5032022 /ug=Hs.25691 /len=1312	NM_005856	Hs.25691	NP_005847
2602	0.042048	fibrinogen-like 2 (FGL2), mRNA /cds=(34,1353) /gb=NM_006682 /gi=5730074 /ug=Hs.351808 /len=1496	NM_006682	Hs.351808	NP_006673
2628	0.003958	methyltransferase reductase (MTRR), transcript variant 2, mRNA /cds=(31,2208) /gb=NM_024010 /gi=13325067 /ug=Hs.153792 /len=3291	NM_024010	Hs.153792	NP_076915
2646	0.031002	EGF-containing fibulin-like extracellular matrix protein 1 (EFEMP1), transcript variant 1, mRNA /cds=(150,1631) /gb=NM_004105 /gi=9665261 /ug=Hs.76224 /len=2742	NM_004105	Hs.76224	NP_061489
2674	0.005206	ring finger protein 10 (RNF10), mRNA /cds=(448,2883) /gb=NM_014868 /gi=27544928 /ug=Hs.5094 /len=3129	NM_014868	Hs.5094	NP_055683
2678	0.031002	protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1), mRNA /cds=(74,757) /gb=NM_005389 /gi=4885538 /ug=Hs.79137 /len=1599	NM_005389	Hs.79137	NP_005380
2681	0.042048	HBS1-like ( <i>S. cerevisiae</i> ) (HBS1L), mRNA /cds=(194,2248) /gb=NM_006620 /gi=24431963 /ug=Hs.221040 /len=7163	NM_006620	Hs.221040	NP_006611
2682	0.016031	choline phosphotransferase 1 (CHPT1), mRNA /cds=(171,1391) /gb=NM_020244 /gi=9910383 /ug=Hs.171889 /len=1536	NM_020244	Hs.171889	NP_064629
2698	0.031002	topoisomerase (DNA) II alpha 170kDa (TOP2A), mRNA /cds=(127,4722) /gb=NM_001067 /gi=19913405 /ug=Hs.156346 /len=5698	NM_001067	Hs.156346	NP_001058
2719	0.014265	HMG-box containing protein 1 (HBP1), mRNA /cds=(187,1731) /gb=NM_012257 /gi=21361410 /ug=Hs.10882 /len=2857	NM_012257	Hs.10882	NP_036389
2729	0.025072	HIC protein isoform p40 and HIC protein isoform p32 mRNAs, complete cds /cds=(264,1331) /gb=AF054589 /gi=3426297 /ug=Hs.132739 /len=4152	AF054589	Hs.132739	
2766	0.008765	sorting nexin 7 (SNX7), transcript variant 1, mRNA /cds=(268,1431) /gb=NM_015976 /gi=23111053 /ug=Hs.127241 /len=1798	NM_015976	Hs.127241	NP_689424

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2784	0.020126	dual specificity phosphatase 14 (DUSP14), mRNA /cds=(234,830) /gb=NM_007026 /gi=5902001 /ug=Hs.91448 /len=1471	NM_007026	Hs.91448	NP_008957
2801	0.027906	Rattus norvegicus mitochondrial genome	NC_001665		
2809	0.020126	cDNA: FLJ21874 fis, clone HEP02488. /gb=AK025527 /gi=10438070 /ug=Hs.208334 /len=2239	AK025527	Hs.208334	
2815	0.022485	proteasome (prosome, macropain) subunit, alpha type, 6 (PSMA6), mRNA /cds=(110,850) /gb=NM_002791 /gi=23110943 /ug=Hs.410276 /len=1035	NM_002791	Hs.410276	NP_002782
2820	0.042048	zinc finger RNA binding protein (ZFR), mRNA /cds=(44,1300) /gb=NM_016107 /gi=7706372 /ug=Hs.173518 /len=2734	NM_016107	Hs.173518	NP_057191
2852	0.042048	prefoldin 4 (PFDN4), mRNA /cds=(1,405) /gb=NM_002623 /gi=12408676 /ug=Hs.91161 /len=1208	NM_002623	Hs.91161	NP_002614
2875	0.034378	deubiquitinating enzyme (UNPH4)= AF153604 ubiquitin-specific protease homolog (UPH)	AF106069		NP_006304
2876	0.034378	transcriptional regulator interacting with the PHS-bromodomain 2 (TRIP-Br2), mRNA /cds=(298,1242) /gb=NM_014755 /gi=7661925 /ug=Hs.77293 /len=5544	NM_014755	Hs.77293	NP_055570
2892	0.042048	t-complex 1 (TCP1), mRNA /cds=(22,1692) /gb=NM_030752 /gi=13540472 /ug=Hs.4112 /len=2019	NM_030752	Hs.4112	NP_110379
2944	0.027906	hypothetical protein FLJ20345 (FLJ20345), mRNA /cds=(175,1425) /gb=NM_017777 /gi=8923323 /ug=Hs.20558 /len=2081	NM_017777	Hs.20558	NP_060247
2945	0.038054	hypothetical protein BC018453 (LOC129531), mRNA /cds=(49,798) /gb=NM_138798 /gi=20270348 /ug=Hs.14222 /len=963	NM_138798	Hs.14222	NP_620153
2958	0.020126	TH1-like (Drosophila) (TH1L), mRNA /cds=(8,1429) /gb=NM_016397 /gi=7705462 /ug=Hs.5184 /len=2130	NM_016397	Hs.5184	NP_057481
2959	0.027906	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) (PIN4), mRNA /cds=(25,420) /gb=NM_006223 /gi=5453901 /ug=Hs.11774 /len=997	NM_006223	Hs.11774	NP_006214

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
2961	0.008765	line-1 protein ORF2 (=p150)	B28096		
3023	0.042048	apolipoprotein D (APOD), mRNA /cds=(62,631) /gb=NM_001647 /gi=4502162 /ug=Hs.75736 /len=809	NM_001647	Hs.75736	NP_001638
3071	0.04638	endothelin receptor type A (EDNRA), mRNA /cds=(485,1768) /gb=NM_001957 /gi=4503464 /ug=Hs.76252 /len=4105	NM_001957	Hs.76252	NP_001948
3072	0.042048	trichorhinophalangeal syndrome I (TRPS1), mRNA /cds=(639,4484) /gb=NM_014112 /gi=7657658 /ug=Hs.26102 /len=10011	NM_014112	Hs.26102	NP_054831
3090	0.025072	Similar to kinesin family member C1, clone MGC:1202 IMAGE:3506669, mRNA, complete cds /cds=(168,2189) /gb=BC000712 /gi=12653842 /ug=Hs.20830 /len=2400	BC000712	Hs.20830	NP_002254
3185	0.020126	mRNA for repressor protein, partial cds. /cds=(1,2157) /gb=D30612 /gi=2723456 /ug=Hs.58167 /len=3737	D30612	Hs.58167	
3202	0.020126	cDNA FLJ13419 fis, clone PLACE1002115. /gb=AK023481 /gi=10435427 /ug=Hs.163443 /len=2290	AK023481	Hs.163443	
3204	0.04638	clone IMAGE:5263531, mRNA /gb=BC037740 /gi=22902216 /ug=Hs.18016 /len=5036	BC037740	Hs.18016	
3241	0.031002	brain specific protein (CGI-38), mRNA /cds=(100,624) /gb=NM_016140 /gi=7706392 /ug=Hs.279772 /len=999	NM_016140	Hs.279772	NP_057224
3280	0.020126	RETROVIRUS-RELATED POL POLYPROTEIN	P11369		
3287	0.031002	FtsJ 1 (E. coli) (FTSJ1), mRNA /cds=(301,1290) /gb=NM_012280 /gi=7110660 /ug=Hs.23170 /len=1867	NM_012280	Hs.23170	NP_803188
3288	0.005206	cyclin G2 (CCNG2), mRNA /cds=(136,1170) /gb=NM_004354 /gi=4757935 /ug=Hs.79069 /len=2044	NM_004354	Hs.79069	NP_004345
3290	0.020126	mitochondrial ribosomal protein L20 (MRPL20), nuclear gene encoding mitochondrial protein, mRNA /cds=(65,514) /gb=NM_017971 /gi=26638656 /ug=Hs.182698 /len=705	NM_017971	Hs.182698	NP_060441
3313	0.025072	ATPase, H transporting, lysosomal 9kDa, V0 subunit e (ATP6V0E), mRNA /cds=(76,321) /gb=NM_003945 /gi=19913435 /ug=Hs.415629 /len=849	NM_003945	Hs.415629	NP_003936

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3322	0.04638	ribonuclease P (30kD) (RPP30), mRNA /cds=(295,1101) /gb=NM_006413 /gi=19923360 /ug=Hs.139120 /len=2643	NM_006413	Hs.139120	NP_006404
3445	0.04638	mRNA; cDNA DKFZp434A1520 (from clone DKFZp434A1520); partial cds /cds=(1,551) /gb=AL137544 /gi=6808224 /ug=Hs.406722 /len=2775	AL137544	Hs.406722	
3520	0.009931	mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /gb=AL080209 /gi=5262698 /ug=Hs.13659 /len=4254	AL080209	Hs.13659	
3524	0.020912	UI-H-DH1-awr-a-12-0-UI.s1 NCI_CGAP_DH1 cDNA clone IMAGE:5893139 3', mRNA sequence /clone=IMAGE:5893139 /clone_end=3' /gb=BQ001533 /gi=19726433 /ug=Hs.194397 /len=1039	BQ001533	Hs.194397	
3539	0.012669	ubiquitin C (UBC), mRNA /cds=(136,2193) /gb=NM_021009 /gi=20149305 /ug=Hs.183704 /len=2309	NM_021009	Hs.183704	NP_066289
3589	0.027906	yeast Sec31p (KIAA0905), mRNA /cds=(54,3716) /gb=NM_014933 /gi=7662369 /ug=Hs.70266 /len=4129	NM_014933	Hs.70266	NP_057295
3616	0.042048	CD1D antigen, d polypeptide (CD1D), mRNA /cds=(165,1172) /gb=NM_001766 /gi=4502648 /ug=Hs.1799 /len=1903	NM_001766	Hs.1799	NP_001757
3649	0.012669	FLJ14680 fis, clone NT2RP2004242, weakly similar to NEUROFILAMENT TRIPLET H PROTEIN /cds=(41,1885) /gb=AK027586 /gi=14042362 /ug=Hs.334802 /len=2551	AK027586	Hs.334802	NP_078994
3672	0.008765	cDNA PSEC0152 fis, clone PLACE1007885. /cds=(20,1144) /gb=AK075459 /gi=22761560 /ug=Hs.350475 /len=2130	AK075459	Hs.350475	
3690	0.027906	IK cytokine, down-regulator of HLA II (IK), mRNA /cds=(112,1785) /gb=NM_006083 /gi=11038650 /ug=Hs.8024 /len=1785	NM_006083	Hs.8024	NP_006074
3693	0.031002	exonuclease GOR (GOR), mRNA /cds=(628,1584) /gb=NM_172239 /gi=26665874 /ug=Hs.373854 /len=6609	NM_172239	Hs.373854	NP_758439

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
3722	0.01798	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J) (CLU), mRNA /cds=(48,1397) /gb=NM_001831 /gi=4502904 /ug=Hs.75106 /len=1676	NM_001831	Hs.75106	NP_001822
3732	0.038054	hypothetical protein FLJ20718 (FLJ20718), mRNA /cds=(228,2012) /gb=NM_017939 /gi=8923644 /ug=Hs.50579 /len=2658	NM_017939	Hs.50579	NP_060409
3763	0.025072	UI-E-EO1-aja-c-22-0-UI.s1 UI-E-EO1 cDNA clone UI-E-EO1-aja-c-22-0-UI 3', mRNA sequence /clone=UI-E-EO1-aja-c-22-0-UI /clone_end=3' /gb=BM680199 /gi=18990095 /ug=Hs.355581 /len=1071	BM680199	Hs.355581	
3802	0.038054	cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307	NM_006371	Hs.155481	NP_006362
3805	0.034378	hypothetical protein FLJ10350 (FLJ10350), mRNA /cds=(676,2340) /gb=NM_018067 /gi=21361780 /ug=Hs.177596 /len=2811	NM_018067	Hs.177596	NP_060537
3889	0.008765	FLJ30635 fis, clone CTONG2002520 /cds=UNKNOWN /gb=AK055197 /gi=16549871 /ug=Hs.351331 /len=2174	AK055197	Hs.351331	NP_000357
3972	0.01798	chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA /cds=(127,1278) /gb=NM_001276 /gi=4557017 /ug=Hs.75184 /len=1925	NM_001276	Hs.75184	NP_001267
4038	0.020126	multiple PDZ domain protein (MPDZ), mRNA /cds=(47,6175) /gb=NM_003829 /gi=4505230 /ug=Hs.169378 /len=6582	NM_003829	Hs.169378	NP_003820
4051	0.04638	methyl CpG binding protein 2 (Rett syndrome) (MECP2), mRNA /cds=(168,1628) /gb=NM_004992 /gi=7710148 /ug=Hs.3239 /len=10182	NM_004992	Hs.3239	NP_004983
4075	0.031002	ankylosis, progressive (mouse) (ANKH), transcript variant 2, mRNA /cds=(265,1743) /gb=NM_054027 /gi=21536394 /ug=Hs.168640 /len=4031	NM_054027	Hs.168640	NP_473368
4082	0.020126	Leu zipper protein p40(61%)	1901303A		1901303A
4084	0.009931	guanyl cyclase C gene,	U20230		
4160	0.031002	BPAG1n3 (BPAG1)	AF165191		NP_065121

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4184	0.012669	ubiquitin-conjugating enzyme E2, J1 (UBC6 yeast) (UBE2J1), mRNA /cds=(118,1095) /gb=NM_016021 /gi=7706311 /ug=Hs.184325 /len=1786	NM_016021	Hs.184325	NP_057420
4199	0.011228	protein phosphatase 1, regulatory subunit 10 (PPP1R10), mRNA /cds=(553,3375) /gb=NM_002714 /gi=25777670 /ug=Hs.106019 /len=4540	NM_002714	Hs.106019	NP_002705
4237	0.042048	smoothelin (SMTN), transcript variant 2, mRNA /cds=(219,2966) /gb=NM_134269 /gi=19913395 /ug=Hs.149098 /len=3294	NM_134269	Hs.149098	NP_599032
4253	0.034374	cartilage associated protein (CRTAP), mRNA /cds=(12,1217) /gb=NM_006371 /gi=21536278 /ug=Hs.155481 /len=2307	NM_006371	Hs.155481	NP_006362
4262	0.006784	peptidylprolyl isomerase B (cyclophilin B) (PPIB), mRNA /cds=(150,800) /gb=NM_000942 /gi=20149505 /ug=Hs.394389 /len=1028	NM_000942	Hs.394389	NP_000933
4264	0.025072	syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component) (SNTA1), mRNA /cds=(273,1790) /gb=NM_003098 /gi=18765742 /ug=Hs.31121 /len=2345	NM_003098	Hs.31121	NP_003089
4307	0.025072	HT015 protein (HT015)	AF223466		NP_061049
4309	0.003958	aminopeptidase puromycin sensitive (NPEPPS), mRNA /cds=(196,2823) /gb=NM_006310 /gi=15451906 /ug=Hs.293007 /len=4177	NM_006310	Hs.293007	NP_006301
4313	0.04638	chromosome 20 open reading frame 167 (C20orf167), mRNA /cds=(64,1053) /gb=NM_052951 /gi=16418440 /ug=Hs.26213 /len=1296	NM_052951	Hs.26213	NP_443183
4349	0.04638	class I cytokine receptor (zcytor5)	AF178684		NP_004741
4389	0.034378	ADP-ribosylation factor 3 (ARF3)	NM_001659		NP_001650
4390	0.027906	ataxia telangiectasia and Rad3 related (ATR), mRNA /cds=(106,8040) /gb=NM_001184 /gi=20143978 /ug=Hs.77613 /len=8265	NM_001184	Hs.77613	NP_001175
4392	0.04638	hypothetical protein MGC14697 (MGC14697), mRNA /cds=(264,440) /gb=NM_032747 /gi=14249375 /ug=Hs.171625 /len=581	NM_032747	Hs.171625	NP_116136



**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4394	0.042048	Likely ortholog of mouse tumor necrosis-alpha-induced adipose-related protein, cDNA FLJ14901 fis, clone PLACE1005409 (AK027807.1)	AK027807	Hs.44208	NP_078912
4404	0.022485	KIAA1723 protein, partial cds /cds=UNKNOWN /gb=AB051510 /gi=12697990 /ug=Hs.8700 /len=7365	AB051510	Hs.8700	NP_006085
4439	0.020126	retinoblastoma binding protein 6 (RBBP6), mRNA /cds=(92,2938) /gb=NM_006910 /gi=5902043 /ug=Hs.91065 /len=2994	NM_006910	Hs.91065	NP_008841
4445	0.038054	cDNA FLJ36681 fis, clone UTERU2006547. /gb=AK094000 /gi=21752972 /ug=Hs.376416 /len=2372	AK094000	Hs.376416	
4452	0.010561	gene from PAC 747L4. /cds=(73,555) /gb=AL035297 /gi=4200248 /ug=Hs.119254 /len=1155	AL035297	Hs.119254	
4453	0.022485	partial RAB18 gene for RAS-related small GTPase RAB18, exons 4-6	AJ277148		
4464	0.025072	suCRase-isomaltase (SI)	M84646		
4468	0.004545	cDNA FLJ13771 fis, clone PLACE4000270. /gb=AK023833 /gi=10435888 /ug=Hs.288934 /len=6133	AK023833	Hs.288934	
4475	0.01798	RNA binding motif protein 8B (RBM8B)	AF231512		
4508	0.04638	peptidyl-prolyl isomerase G (cyclophilin G) (PPIG), mRNA /cds=(158,2422) /gb=NM_004792 /gi=4758105 /ug=Hs.77965 /len=2695	NM_004792	Hs.77965	NP_004783
4514	0.038054	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 2 (MLLT2) =L13773, AF-4 mRNA,	NM_005935		NP_005926
4515	0.04638	cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA /cds=(408,3872) /gb=NM_033655 /gi=16306508 /ug=Hs.212839 /len=5017	NM_033655	Hs.212839	NP_387504
4521	0.04638	zinc finger protein 267 (ZNF267), transcript variant 498723, mRNA /cds=(134,2365) /gb=NM_003414 /gi=24431954 /ug=Hs.145498 /len=3205	NM_003414	Hs.145498	NP_003405
4548	0.038054	type II integral membrane protein (NKG2-D) (=U08988 CRFB4 )	AF001297		

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4550	0.008765	hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) (HPRT1), mRNA /cds=(86,742) /gb=NM_000194 /gi=4504482 /ug=Hs.82314 /len=1331	NM_000194	Hs.82314	NP_000185
4567	0.00772	CD163 antigen (CD163), mRNA /cds=(102,3572) /gb=NM_004244 /gi=19923275 /ug=Hs.74076 /len=4950	NM_004244	Hs.74076	NP_004235
4584	0.012669	Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA /cds=(1,4065) /gb=NM_005406 /gi=4885582 /ug=Hs.17820 /len=4065	NM_005406	Hs.17820	NP_005397
4590	0.016031	zinc finger protein 106 (ZFP106), mRNA /cds=(336,5987) /gb=NM_022473 /gi=11968022 /ug=Hs.15220 /len=10487	NM_022473	Hs.15220	NP_071918
4595	0.027906	wc09c01.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2314656 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR mRNA sequence /clone=IMAGE:2314656 /clone_end=3' /gb=AI674177 /gi=4874657 /ug=Hs.200089 /len=526	AI674177	Hs.200089	
4614	0.038054	sperm antigen-36	AF187554		
4634	0.034378	DNAJ domain-containing (MCJ), mRNA /cds=(424,876) /gb=NM_013238 /gi=7019452 /ug=Hs.45105 /len=1074	NM_013238	Hs.45105	NP_037370
4661	0.005206	cDNA FLJ30561 fis, clone BRAWH2004580. /gb=AK055123 /gi=16549782 /ug=Hs.153618 /len=2115	AK055123	Hs.153618	
4668	0.027906	cDNA FLJ31439 fis, clone NT2NE2000707. /gb=AK056001 /gi=16550873 /ug=Hs.349656 /len=2009	AK056001	Hs.349656	
4680	0.011228	U4/U6-associated RNA splicing factor (HPRP3P), mRNA /cds=(73,2124) /gb=NM_004698 /gi=4758555 /ug=Hs.11776 /len=2344	NM_004698	Hs.11776	NP_004689
4689	0.025072	t-complex-associated-testis-expressed 1-like (TCTE1L), mRNA /cds=(69,419) /gb=NM_006520 /gi=5730086 /ug=Hs.446392 /len=2156	NM_006520	Hs.446392	NP_006511

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
4798	0.022485	Rho-associated, coiled-coil containing protein kinase 2 (ROCK2), mRNA /cds=(455,4621) /gb=NM_004850 /gi=6633807 /ug=Hs.58617 /len=6409	NM_004850	Hs.58617	NP_004841
4800	0.022485	COP9 constitutive photomorphogenic subunit 4 (Arabidopsis) (COPS4), mRNA /cds=(7,1224) /gb=NM_016129 /gi=7705844 /ug=Hs.6671 /len=1613	NM_016129	Hs.6671	NP_057213
4821	0.042048	eukaryotic translation termination factor 1 (ETF1), mRNA /cds=(136,1449) /gb=NM_004730 /gi=4759033 /ug=Hs.77324 /len=3653	NM_004730	Hs.77324	NP_004721
4855	0.042048	KIAA0795 protein(KIAA0795), mRNA	XM_016166		
4873	0.01798	LAT1-3TM protein (LAT1-3TM), mRNA /cds=(80,622) /gb=NM_031211 /gi=13654279 /ug=Hs.325520 /len=2114	NM_031211	Hs.325520	NP_112488
4992	0.034378	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) (TFPI), mRNA /cds=(1,915) /gb=NM_006287 /gi=6715569 /ug=Hs.170279 /len=915	NM_006287	Hs.170279	NP_006278
5033	0.031002	actin related protein 2/3 complex, subunit 2, 34kDa (ARPC2), transcript variant 1, mRNA /cds=(113,1015) /gb=NM_152862 /gi=23238210 /ug=Hs.83583 /len=1462	NM_152862	Hs.83583	NP_690601
5072	0.008765	actin binding LIM protein 2 (ABLM2), mRNA /cds=(123,1718) /gb=NM_032432 /gi=27477050 /ug=Hs.25522 /len=3407	NM_032432	Hs.25522	NP_115808
5082	0.042048	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 2 (SLC9A3R2), mRNA /cds=(97,1449) /gb=NM_004785 /gi=4759141 /ug=Hs.101813 /len=1600	NM_004785	Hs.101813	NP_004776
5177	0.031002	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa (EIF3S10), mRNA /cds=(114,4262) /gb=NM_003750 /gi=4503508 /ug=Hs.154796 /len=5256	NM_003750	Hs.154796	NP_003741
5183	0.012669	basic transCRiption factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn)	U80017		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5184	0.016031	ankyrin repeat, family A (RFXANK-like), 2 (ANKRA2), mRNA /cds=(648,1589) /gb=NM_023039 /gi=21362082 /ug=Hs.239154 /len=2048	NM_023039	Hs.239154	NP_075526
5188	0.020126	p53R2 mRNA for ribonucleotide reductase, complete cds. /cds=(245,1300) /gb=AB036063 /gi=7229085 /ug=Hs.94262 /len=4955	AB036063	Hs.94262	
5204	0.020126	stathmin-like 3 (STMN3), mRNA /cds=(83,625) /gb=NM_015894 /gi=14670374 /ug=Hs.285753 /len=2255	NM_015894	Hs.285753	NP_056978
5246	0.04638	cNA sequence (RC2-BT0389-010400-013-e04 BT0389)	BE069597		NP_001675
5267	0.034378	RNA binding motif protein 6 (RBM6), mRNA /cds=(134,3505) /gb=NM_005777 /gi=5032032 /ug=Hs.173993 /len=3639	NM_005777	Hs.173993	NP_005768
5273	0.014265	mRNA; cDNA DKFZp434A163 (from clone DKFZp434A163); partial cds /cds=(1,4964) /gb=AL110218 /gi=5817150 /ug=Hs.127401 /len=5084	AL110218	Hs.127401	
5279	0.031002	paternally expressed 10 (PEG10), mRNA /cds=(118,1095) /gb=NM_015068 /gi=14149662 /ug=Hs.137476 /len=6253	NM_015068	Hs.137476	NP_055883
5320	0.025072	mRNA; cDNA DKFZp564O0122 (from clone DKFZp564O0122) /gb=AL049951 /gi=4884198 /ug=Hs.22370 /len=1727	AL049951	Hs.22370	
5328	0.011228	CDC20 cell division cycle 20 (S. cerevisiae) (CDC20), mRNA /cds=(111,1610) /gb=NM_001255 /gi=4557436 /ug=Hs.82906 /len=1686	NM_001255	Hs.82906	NP_001246
5349	0.042048	peroxisome receptor 1 (PXR1), mRNA /cds=(52,1947) /gb=NM_000319 /gi=21361203 /ug=Hs.158084 /len=3227	NM_000319	Hs.158084	NP_000310
5388	0.016031	peroxiredoxin 1 (PRDX1), mRNA /cds=(61,660) /gb=NM_002574 /gi=4505590 /ug=Hs.180909 /len=937	NM_002574	Hs.180909	NP_002565
5394	0.005949	hypothetical protein FLJ11294 (FLJ11294), mRNA /cds=(160,4170) /gb=NM_018383 /gi=19923528 /ug=Hs.107000 /len=4602	NM_018383	Hs.107000	NP_060853

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5399	0.042048	cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA /cds=(466,1062) /gb=NM_004064 /gi=17978497 /ug=Hs.238990 /len=2422	NM_004064	Hs.238990	NP_004055
5400	0.042048	dUTP pyrophosphatase (DUT), mRNA /cds=(20,514) /gb=NM_001948 /gi=21361335 /ug=Hs.367676 /len=1816	NM_001948	Hs.367676	NP_001939
5414	0.027906	mRNA; cDNA DKFZp313L1834 (from clone DKFZp313L1834) /gb=AL832699 /gi=21733278 /ug=Hs.336446 /len=2883	AL832699	Hs.336446	
5426	0.04638	Hypothetical protein(cDNA: FLJ23458 fis, clone HSI07327)	AK027111		NP_000976
5428	0.042048	proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7), mRNA /cds=(18,851) /gb=NM_002799 /gi=23110926 /ug=Hs.433434 /len=1012	NM_002799	Hs.433434	NP_002790
5453	0.031002	nuclear factor (erythroid-derived 2)-like 2 (NFE2L2), mRNA /cds=(114,1931) /gb=NM_006164 /gi=20149575 /ug=Hs.155396 /len=2439	NM_006164	Hs.155396	NP_006155
5489	0.027906	DKFZP566H073 protein (DKFZP566H073), mRNA /cds=(450,1502) /gb=NM_015528 /gi=14149701 /ug=Hs.7158 /len=1723	NM_015528	Hs.7158	NP_056343
5505	0.027906	SECIS binding protein 2 (SBP2), mRNA /cds=(58,2622) /gb=NM_024077 /gi=21359954 /ug=Hs.288141 /len=3457	NM_024077	Hs.288141	NP_076982
5519	0.012669	solute carrier family 4, sodium bicarbonate cotransporter, member 7 (SLC4A7), mRNA /cds=(72,3716) /gb=NM_003615 /gi=19923175 /ug=Hs.132904 /len=7785	NM_003615	Hs.132904	NP_003606
5522	0.031002	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B) (TCEB2), mRNA /cds=(1,357) /gb=NM_007108 /gi=6005889 /ug=Hs.172772 /len=357	NM_007108	Hs.172772	NP_009039
5525	0.042048	tuftelin interacting protein 11 (TFIP11), mRNA /cds=(264,2777) /gb=NM_012143 /gi=8393258 /ug=Hs.20225 /len=3565	NM_012143	Hs.20225	NP_036275

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
5529	0.031002	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2 (SMARCD2), mRNA /cds=(423,1850) /gb=NM_003077 /gi=21264350 /ug=Hs.250581 /len=2704	NM_003077	Hs.250581	NP_003068
5560	0.04638	insulin-like growth factor 2 receptor (IGF2R), mRNA /cds=(148,7623) /gb=NM_000876 /gi=4504610 /ug=Hs.76473 /len=9090	NM_000876	Hs.76473	NP_000867
5562	0.034378	high-mobility group box 2 (HMGB2), mRNA /cds=(191,820) /gb=NM_002129 /gi=14141173 /ug=Hs.80684 /len=1277	NM_002129	Hs.80684	NP_002120
5596	0.01798	CDA02 protein (CDA02), mRNA /cds=(3,1832) /gb=NM_032025 /gi=14042940 /ug=Hs.332404 /len=2179	NM_032025	Hs.332404	NP_114414
5605	0.027906	GABA(A) receptor-associated protein-like 2 (GABARAPL2), mRNA /cds=(137,490) /gb=NM_007285 /gi=27374999 /ug=Hs.6518 /len=1031	NM_007285	Hs.6518	NP_009216
5665	0.020126	golgi associated, gamma adaptin ear containing, ARF binding protein 3 (GGA3), transcript variant long, mRNA /cds=(10,2181) /gb=NM_138619 /gi=20336266 /ug=Hs.87726 /len=3860	NM_138619	Hs.87726	NP_619525
5827	0.00772	PHKB gene (exon 25)	X84930		
5905	0.020126	protein phosphatase 2 (formerly 2A), regulatory subunit B", alpha (PPP2R3A), mRNA /cds=(505,3957) /gb=NM_002718 /gi=19923228 /ug=Hs.28219 /len=5217	NM_002718	Hs.28219	NP_002709
5906	0.038054	602034564F1 NCI_CGAP_Brn64 cDNA clone IMAGE:4182759 5', mRNA sequence /clone=IMAGE:4182759 /clone_end=5' /gb=BF337136 /gi=11283240 /ug=Hs.398001 /len=1223	BF337136	Hs.398001	
5934	0.012669	enthoprotin (ENTH), mRNA /cds=(102,1979) /gb=NM_014666 /gi=7661967 /ug=Hs.132853 /len=3336	NM_014666	Hs.132853	NP_055481
5986	0.006784	zinc finger and BTB domain containing 1 (ZBTB1), mRNA /cds=(263,2197) /gb=NM_014950 /gi=7662437 /ug=Hs.372699 /len=3990	NM_014950	Hs.372699	NP_055765

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6026	0.022485	fibromodulin (FMOD), mRNA /cds=(21,1151) /gb=NM_002023 /gi=5016093 /ug=Hs.230 /len=2863	NM_002023	Hs.230	NP_002014
6040	0.00772	von Hippel-Lindau binding protein 1 (VBP1), mRNA /cds=(211,804) /gb=NM_003372 /gi=21614497 /ug=Hs.198307 /len=1778	NM_003372	Hs.198307	NP_003363
6125	0.04638	Sjogren's syndrome nuclear autoantigen 1 (SSNA1), mRNA /cds=(47,406) /gb=NM_003731 /gi=4505324 /ug=Hs.18528 /len=865	NM_003731	Hs.18528	NP_003722
6127	0.006784	zinc finger protein 76 (expressed in testis) (ZNF76), mRNA /cds=(215,1927) /gb=NM_003427 /gi=21361145 /ug=Hs.29222 /len=2680	NM_003427	Hs.29222	NP_003418
6128	0.014265	Rab acceptor 1 (prenylated) (RABAC1), mRNA /cds=(31,588) /gb=NM_006423 /gi=5453959 /ug=Hs.11417 /len=770	NM_006423	Hs.11417	NP_006414
6131	0.016031	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa (NDUFA8), mRNA /cds=(68,586) /gb=NM_014222 /gi=7657368 /ug=Hs.31547 /len=700	NM_014222	Hs.31547	NP_055037
6135	0.005206	cyclin-dependent kinase 4 (CDK4), transcript variant 1, mRNA /cds=(228,1139) /gb=NM_000075 /gi=16936531 /ug=Hs.95577 /len=1474	NM_000075	Hs.95577	NP_443710
6137	0.038054	developmentally regulated GTP binding protein 2 (DRG2), mRNA /cds=(65,1159) /gb=NM_001388 /gi=23065518 /ug=Hs.78582 /len=1897	NM_001388	Hs.78582	NP_001379
6143	0.035996	mRNA; cDNA DKFZp686G1167 (from clone DKFZp686G1167) /gb=AL833600 /gi=21734246 /ug=Hs.7720 /len=8355	AL833600	Hs.7720	NP_001367
6180	0.038054	mRNA for KIAA0774 protein, partial cds. /cds=(1,3492) /gb=AB018317 /gi=3882268 /ug=Hs.22201 /len=4021	AB018317	Hs.22201	
6215	0.027906	splicing factor, arginine/serine-rich 2 (SFRS2), mRNA /cds=(156,821) /gb=NM_003016 /gi=4506898 /ug=Hs.73965 /len=1879	NM_003016	Hs.73965	NP_003007
6227	0.027906	splicing factor, arginine/serine-rich 4 (SFRS4), mRNA /cds=(107,1591) /gb=NM_005626 /gi=21361281 /ug=Hs.76122 /len=2167	NM_005626	Hs.76122	NP_005617

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6230	0.029136	nudix (nucleoside diphosphate linked moiety X)-type motif 4 (NUDT4), mRNA /cds=(191,736) /gb=NM_019094 /gi=24432097 /ug=Hs.355399 /len=3652	NM_019094	Hs.355399	NP_061967
6256	0.020126	ribonuclease, RNase A family, 4 (RNASE4), mRNA /cds=(173,616) /gb=NM_002937 /gi=20070170 /ug=Hs.283749 /len=1414	NM_002937	Hs.283749	NP_002928
6263	0.034378	down-regulated in metastasis (DRIM), mRNA /cds=(145,8502) /gb=NM_014503 /gi=7657040 /ug=Hs.178614 /len=9017	NM_014503	Hs.178614	NP_055318
6307	0.035996	cDNA FLJ37296 fis, clone BRAMY2015420. /gb=AK094615 /gi=21753707 /ug=Hs.4983 /len=3181	AK094615	Hs.4983	
6316	0.048742	KIAA1046 protein (KIAA1046)	NM_014928		
6324	0.025072	SR rich protein (DKFZp564B0769), mRNA /cds=(33,2450) /gb=NM_032870 /gi=18699723 /ug=Hs.18368 /len=2663	NM_032870	Hs.18368	NP_116259
6325	0.027906	AT-binding transcription factor 1 (ATBF1), mRNA /cds=(674,11785) /gb=NM_006885 /gi=19923286 /ug=Hs.101842 /len=11893	NM_006885	Hs.101842	NP_008816
6347	0.038054	mitochondrion, complete genome	NC_001807		
6367	0.01798	growth arrest-specific 1 (GAS1), mRNA /cds=(411,1448) /gb=NM_002048 /gi=4503918 /ug=Hs.65029 /len=2828	NM_002048	Hs.65029	NP_002039
6378	0.04638	signal peptidase complex (18kD) (SPC18), mRNA /cds=(78,617) /gb=NM_014300 /gi=7657608 /ug=Hs.9534 /len=1105	NM_014300	Hs.9534	NP_055115
6387	0.031002	epithelial protein lost in neoplasm beta (EPLIN), mRNA /cds=(102,2381) /gb=NM_016357 /gi=7705372 /ug=Hs.10706 /len=3655	NM_016357	Hs.10706	NP_057441
6419	0.016031	RNA helicase family (RNAH), mRNA /cds=(39,6647) /gb=NM_006828 /gi=24307916 /ug=Hs.48295 /len=7315	NM_006828	Hs.48295	NP_006819
6422	0.012669	soc-2 suppressor of clear (C. elegans) (SHOC2), mRNA /cds=(278,2026) /gb=NM_007373 /gi=6677944 /ug=Hs.104315 /len=3872	NM_007373	Hs.104315	NP_031399
6466	0.034378	ralA binding protein 1 (RALBP1), mRNA /cds=(78,2045) /gb=NM_006788 /gi=21361362 /ug=Hs.75447 /len=4230	NM_006788	Hs.75447	NP_006779



TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6468	0.034378	reverse transcriptase related protein	1207289A		1207289A
6471	0.042048	hydroxysteroid (11-beta) dehydrogenase 1 (HSD11B1), mRNA /cds=(95,973) /gb=NM_005525 /gi=5031764 /ug=Hs.275215 /len=1375	NM_005525	Hs.275215	NP_005516
6477	0.012669	NIMA (never in mitosis gene a)-related kinase 7, DKFZp586G2222 (from clone DKFZp586G2222) (AL080111.1)	AL080111	Hs.24119	NP_598001
6498	0.006784	keratinocyte, normal	U33270		
6608	0.027906	mitogen-activated protein kinase 14 (MAPK14), transcript variant 2, mRNA /cds=(363,1445) /gb=NM_139012 /gi=20986511 /ug=Hs.79107 /len=3757	NM_139012	Hs.79107	NP_620583
6609	0.038054	fibroblast growth factor 2 (basic) (FGF2), mRNA /cds=(302,934) /gb=NM_002006 /gi=15451897 /ug=Hs.284244 /len=6802	NM_002006	Hs.284244	NP_001997
6610	0.027906	Similar to RIKEN cDNA 3830613O22 gene, clone IMAGE:5551209, mRNA, partial cds /cds=(282,4079) /gb=BC035645 /gi=23272851 /ug=Hs.356876 /len=4079	BC035645	Hs.356876	
6640	0.034378	c6.1A (C6.1A), mRNA /cds=(3,953) /gb=NM_024332 /gi=13236582 /ug=Hs.301927 /len=2846	NM_024332	Hs.301927	NP_077308
6714	0.025072	chromosome 20 open reading frame 43 (C20orf43), mRNA /cds=(71,991) /gb=NM_016407 /gi=7705482 /ug=Hs.182281 /len=1639	NM_016407	Hs.182281	NP_057491
6715	0.038054	KIAA0076 gene product (KIAA0076), mRNA /cds=(87,5183) /gb=NM_014780 /gi=7661893 /ug=Hs.51039 /len=5253	NM_014780	Hs.51039	NP_055595
6718	0.022485	nucleoporin 210 (NUP210), mRNA /cds=(84,5747) /gb=NM_024923 /gi=27477133 /ug=Hs.270404 /len=7191	NM_024923	Hs.270404	NP_079199
6722	0.022485	syndecan 1 (SDC1), mRNA /cds=(253,1185) /gb=NM_002997 /gi=21359855 /ug=Hs.82109 /len=2484	NM_002997	Hs.82109	NP_002988
6836	0.025072	UI-E-DW1-ahd-d-13-0-UI.s1 UI-E-DW1 cDNA clone UI-E-DW1-ahd-d-13-0-UI 3', mRNA sequence /clone=UI-E-DW1-ahd-d-13-0-UI /clone_end=3' /gb=BU737702 /gi=23673914 /ug=Hs.405983 /len=1215	BU737702	Hs.405983	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
6847	0.031002	tropomodulin 3 (ubiquitous) (TMOD3), mRNA /cds=(66,1124) /gb=NM_014547 /gi=7657648 /ug=Hs.22826 /len=2072	NM_014547	Hs.22826	NP_055362
6853	0.042048	DKFZp434K098 (from clone DKFZp434K098); partial cds	AL133112		NP_653172
6898	0.038054	plexin B2 (PLXNB2), mRNA /cds=(26,1438) /gb=NM_012401 /gi=20270189 /ug=Hs.3989 /len=2175	NM_012401	Hs.3989	NP_036533
6908	0.00772	thymus expressed gene 3-like (MGC15476), mRNA /cds=(441,1655) /gb=NM_145056 /gi=21450823 /ug=Hs.134185 /len=2544	NM_145056	Hs.134185	NP_659493
6942	0.020126	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
7003	0.004545	histocompatibility (minor) 13 (HM13), mRNA /cds=(86,1219) /gb=NM_030789 /gi=23308606 /ug=Hs.386538 /len=1584	NM_030789	Hs.386538	NP_848697
7041	0.012669	oxysterol binding protein-like 1A (OSBPL1A), transcript variant OSBPL1B, mRNA /cds=(175,3027) /gb=NM_080597 /gi=19718740 /ug=Hs.252716 /len=4165	NM_080597	Hs.252716	NP_579802
7048	0.038054	twisted gastrulation 1 (Drosophila) (TWSG1), mRNA /cds=(106,777) /gb=NM_020648 /gi=21314788 /ug=Hs.247302 /len=3693	NM_020648	Hs.247302	NP_065699
7064	0.020126	mitochondrial ribosomal protein L18 (MRPL18), nuclear gene encoding mitochondrial protein, mRNA /cds=(123,665) /gb=NM_014161 /gi=21265079 /ug=Hs.23038 /len=989	NM_014161	Hs.23038	NP_054880
7092	0.00772	chromosome condensation 1 (CHC1), mRNA /cds=(287,1552) /gb=NM_001269 /gi=20149512 /ug=Hs.84746 /len=2559	NM_001269	Hs.84746	NP_001260
7103	0.042048	sialidase 1 (lysosomal sialidase) (NEU1), mRNA /cds=(130,1377) /gb=NM_000434 /gi=4557790 /ug=Hs.118721 /len=1894	NM_000434	Hs.118721	NP_000425
7112	0.027906	ubiquitination factor E4A (UFD2 yeast) (UBE4A), mRNA /cds=(73,3294) /gb=NM_004788 /gi=4759287 /ug=Hs.75275 /len=6060	NM_004788	Hs.75275	NP_004779

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7127	0.011228	actin-related protein 10 ( <i>S. cerevisiae</i> ) (ACTR10), mRNA /cds=(81,1334) /gb=NM_018477 /gi=8923711 /ug=Hs.274369 /len=1621	NM_018477	Hs.274369	NP_060947
7143	0.04638	benzodiazapine receptor (peripheral) (BZRP), nuclear gene encoding mitochondrial protein, transcript variant PBR, mRNA /cds=(88,597) /gb=NM_000714 /gi=21536444 /ug=Hs.202 /len=848	NM_000714	Hs.202	NP_009295
7147	0.038054	UI-1-BB1p-aki-h-05-0-UI.s1 NCI_CGAP_PI6 cDNA clone UI-1-BB1p-aki-h-05-0-UI 3', mRNA sequence /clone=UI-1-BB1p-aki-h-05-0-UI /clone_end=3' /gb=BQ022477 /gi=19757756 /ug=Hs.424771 /len=1598	BQ022477	Hs.424771	
7203	0.031002	KIAA1036 protein (KIAA1036), mRNA /cds=(386,1483) /gb=NM_014909 /gi=7662453 /ug=Hs.155182 /len=5481	NM_014909	Hs.155182	NP_055724
7204	0.031002	chromosome 20 open reading frame 98 (C20orf98), mRNA /cds=(134,748) /gb=NM_024958 /gi=13376446 /ug=Hs.286128 /len=2042	NM_024958	Hs.286128	NP_079234
7205	0.042048	ribosomal protein S20 (RPS20), mRNA /cds=(128,487) /gb=NM_001023 /gi=14591915 /ug=Hs.8102 /len=539	NM_001023	Hs.8102	NP_001014
7250	0.038054	hemoglobin, gamma G (HBG2), mRNA /cds=(54,497) /gb=NM_000184 /gi=28302132 /ug=Hs.386655 /len=583	NM_000184	Hs.386655	NP_000175
7292	0.025072	synaptic nuclei expressed gene 1 (SYNE-1), transcript variant beta, mRNA /cds=(121,10086) /gb=NM_015293 /gi=19526752 /ug=Hs.192102 /len=10742	NM_015293	Hs.192102	NP_598411
7322	0.038054	BM-017 (=ALEX3)	AF208859		NP_808817
7349	0.027906	dermatopontin (DPT), mRNA /cds=(7,612) /gb=NM_001937 /gi=4755134 /ug=Hs.80552 /len=717	NM_001937	Hs.80552	NP_001928
7355	0.038054	hypothetical protein (DKFZp761P2124 clone DKFZp761P2124)	AL137441		NP_057107
7361	0.031002	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4), mRNA /cds=(277,5220) /gb=NM_003072 /gi=21071055 /ug=Hs.78202 /len=5681	NM_003072	Hs.78202	NP_003063

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7366	0.027906	meningioma expressed antigen 5 (hyaluronidase) (MGEA5), mRNA /cds=(396,3146) /gb=NM_012215 /gi=11024697 /ug=Hs.5734 /len=5147	NM_012215	Hs.5734	NP_036347
7382	0.04638	cortactin binding protein 2 (CORTBP2), mRNA /cds=(93,5084) /gb=NM_033427 /gi=16975495 /ug=Hs.293539 /len=5975	NM_033427	Hs.293539	NP_219499
7383	0.042048	mannose receptor, C type 1 (MRC1), mRNA /cds=(104,4474) /gb=NM_002438 /gi=4505244 /ug=Hs.75182 /len=5185	NM_002438	Hs.75182	NP_002429
7398	0.034378	laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA /cds=(50,9382) /gb=NM_000426 /gi=4557708 /ug=Hs.75279 /len=9534	NM_000426	Hs.75279	NP_000417
7415	0.04638	hypothetical protein FLJ12619 (FLJ12619), mRNA /cds=(539,1228) /gb=NM_030939 /gi=21359961 /ug=Hs.7779 /len=2444	NM_030939	Hs.7779	NP_112201
7427	0.034378	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
7455	0.04638	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2), mRNA /cds=(67,903) /gb=NM_006412 /gi=6041664 /ug=Hs.209119 /len=1522	NM_006412	Hs.209119	NP_006403
7459	0.020126	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 (PSMD13), mRNA /cds=(70,1200) /gb=NM_002817 /gi=4506222 /ug=Hs.279554 /len=1584	NM_002817	Hs.279554	NP_787128
7461	0.020126	dipeptidase 1 (renal) (DPEP1), mRNA /cds=(296,1531) /gb=NM_004413 /gi=4758189 /ug=Hs.109 /len=1738	NM_004413	Hs.109	NP_004404
7466	0.00772	ret finger protein (RFP), transcript variant alpha, mRNA /cds=(359,1900) /gb=NM_006510 /gi=17105396 /ug=Hs.142653 /len=2984	NM_006510	Hs.142653	NP_112212
7495	0.034378	CASP8 and FADD-like apoptosis regulator (CFLAR), mRNA /cds=(482,1924) /gb=NM_003879 /gi=21361768 /ug=Hs.195175 /len=2243	NM_003879	Hs.195175	NP_003870

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7514	0.04638	cDNA FLJ35055 fis, clone OCBBF2018563. /gb=AK092374 /gi=21750952 /ug=Hs.349303 /len=3817	AK092374	Hs.349303	
7517	0.00772	deoxyguanosine kinase (DGUOK), transcript variant 1, nuclear gene encoding mitochondrial protein, mRNA /cds=(86,919) /gb=NM_080916 /gi=18426966 /ug=Hs.432811 /len=1144	NM_080916	Hs.432811	NP_550440
7522	0.016031	TH1-like (Drosophila) (TH1L), mRNA /cds=(8,1429) /gb=NM_016397 /gi=7705462 /ug=Hs.5184 /len=2130	NM_016397	Hs.5184	NP_057481
7532	0.04638	a disintegrin and metalloproteinase domain 33 (ADAM33), transcript variant 1, mRNA /cds=(88,2529) /gb=NM_025220 /gi=24041037 /ug=Hs.173716 /len=3594	NM_025220	Hs.173716	NP_694882
7544	0.039654	oxysterol binding protein-like 10 (OSBPL10), mRNA /cds=(382,2676) /gb=NM_017784 /gi=23111057 /ug=Hs.321622 /len=3938	NM_017784	Hs.321622	NP_060254
7549	0.00772	cDNA: FLJ21552 fis, clone COL06322. /gb=AK025205 /gi=10437670 /ug=Hs.6634 /len=2045	AK025205	Hs.6634	
7550	0.00772	hypothetical protein FLJ20343 (FLJ20343), mRNA /cds=(19,1524) /gb=NM_017775 /gi=22547158 /ug=Hs.252692 /len=2784	NM_017775	Hs.252692	NP_060245
7551	0.025072	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA /cds=(767,1375) /gb=NM_023012 /gi=20127619 /ug=Hs.81648 /len=1878	NM_023012	Hs.81648	NP_075388
7552	0.006784	interferon, alpha-inducible protein (clone IFI-15K) (G1P2), mRNA /cds=(76,573) /gb=NM_005101 /gi=4826773 /ug=Hs.432233 /len=634	NM_005101	Hs.432233	NP_005092
7574	0.023403	ubiquitin-conjugating enzyme E2N (UBC13 yeast) (UBE2N), mRNA /cds=(64,522) /gb=NM_003348 /gi=4507792 /ug=Hs.75355 /len=1203	NM_003348	Hs.75355	NP_003339
7613	0.034378	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7620	0.027906	UI-H-EI0-ayf-a-03-0-UI.s1 NCI_CGAP_EI0 cDNA clone UI-H-EI0-ayf-a-03-0-UI 3', mRNA sequence /clone=UI-H-EI0-ayf-a-03-0-UI /clone_end=3' /gb=CA447644 /gi=24812064 /ug=Hs.440691 /len=770	CA447644	Hs.440691	
7628	0.014265	FLJ10287 fis, clone HEMBB1001387	AK001149		NP_061956
7631	0.031002	mRNA for KIAA0794 protein, partial cds. /cds=(1,1473) /gb=AB018337 /gi=3882308 /ug=Hs.127287 /len=4656	AB018337	Hs.127287	
7649	0.031002	cDNA FLJ20709 fis, clone KAIA1124, highly similar to D86324 mRNA for CMP-N-acetylneuraminic acid. /gb=AK000716 /gi=7020978 /ug=Hs.24697 /len=3488	AK000716	Hs.24697	
7664	0.04638	hypothetical protein DKFZp761J139 (DKFZp761J139), mRNA /cds=(3155,3970) /gb=NM_032280 /gi=14150026 /ug=Hs.15536 /len=4635	NM_032280	Hs.15536	NP_115656
7667	0.031002	cDNA FLJ31147 fis, clone IMR322001438. /gb=AK055709 /gi=16550504 /ug=Hs.6670 /len=1747	AK055709	Hs.6670	
7694	0.034378	cDNA FLJ25013 fis, clone CBL01365. /gb=AK057742 /gi=16553667 /ug=Hs.380091 /len=2200	AK057742	Hs.380091	
7696	0.034378	glycine receptor, beta (GLRB), mRNA /cds=(142,1635) /gb=NM_000824 /gi=24431943 /ug=Hs.32973 /len=2649	NM_000824	Hs.32973	NP_000815
7700	0.00772	mRNA; cDNA DKFZp564B222 (from clone DKFZp564B222) /gb=AL049974 /gi=4884224 /ug=Hs.100261 /len=2315	AL049974	Hs.100261	
7704	0.005949	solute carrier family 35 (CMP-sialic acid transporter), member 1 (SLC35A1), mRNA /cds=(28,1041) /gb=NM_006416 /gi=20149579 /ug=Hs.82921 /len=1883	NM_006416	Hs.82921	NP_006407
7715	0.027906	yw32d06.s1 Morton Fetal Cochlea cDNA clone IMAGE:253931 3', mRNA sequence /clone=IMAGE:253931 /clone_end=3' /gb=N22084 /gi=1128218 /ug=Hs.440534 /len=230	N22084	Hs.440534	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7719	0.038054	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA /cds=(394,1488) /gb=NM_057159 /gi=16950637 /ug=Hs.75794 /len=2732	NM_057159	Hs.75794	NP_476500
7732	0.014265	hypothetical protein FLJ20265 (FLJ20265), mRNA /cds=(40,1854) /gb=NM_017733 /gi=8923239 /ug=Hs.7099 /len=2039	NM_017733	Hs.7099	NP_060203
7739	0.009931	hypothetical protein MGC12458 (MGC12458), mRNA /cds=(30,518) /gb=NM_032328 /gi=14150107 /ug=Hs.330664 /len=1026	NM_032328	Hs.330664	NP_115704
7740	0.00344	tripartite motif-containing 32 (TRIM32), mRNA /cds=(134,2095) /gb=NM_012210 /gi=15208649 /ug=Hs.236218 /len=3160	NM_012210	Hs.236218	NP_036342
7748	0.031002	Hypothetical protein HSPC232, clone IMAGE:4893383, mRNA, partial cds /cds=UNKNOWN /gb=BC025306 /gi=19263704 /ug=Hs.281428 /len=3392	BC025306	Hs.281428	NP_057572
7751	0.012669	Leishmanolysin-like (metallopeptidase M8 family), cDNA /clone=CS0DF004YF03 /gb=AL565471 /gi=12916880 /ug=Hs.90363 /len=1028	AL565471	Hs.90363	NP_149018
7755	0.005206	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA /cds=(44,2248) /gb=NM_003798 /gi=4503128 /ug=Hs.58488 /len=2446	NM_003798	Hs.58488	NP_003789
7758	0.020126	mRNA for KIAA0527 protein, partial cds. /cds=(1,2308) /gb=AB011099 /gi=3043577 /ug=Hs.196647 /len=5005	AB011099	Hs.196647	
7774	0.008765	leucine-rich repeat-containing 5 (LRR5), mRNA /cds=(917,2965) /gb=NM_018103 /gi=24431980 /ug=Hs.44672 /len=3338	NM_018103	Hs.44672	NP_060573
7775	0.031002	fibronectin gene ED-A region	X07718		
7791	0.01798	brain cell membrane protein 1 (BCMP1), mRNA /cds=(10,555) /gb=NM_031442 /gi=13899272 /ug=Hs.8769 /len=3803	NM_031442	Hs.8769	NP_113630
7803	0.011228	EST(yi82d03.s1 Soares placenta Nb2HP clone IMAGE:145733 3' gb:D00762 PROTEASOME COMPONENT C8)	R77952		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7826	0.022485	yh68a05.s1 Soares placenta Nb2HP cDNA clone IMAGE:134864 3', mRNA sequence /clone=IMAGE:134864 /clone_end=3' /gb=R32301 /gi=788144 /ug=Hs.386871 /len=246	R32301	Hs.386871	
7828	0.025072	BX101939 Soares infant brain 1NIB cDNA clone IMAGp998C11163, mRNA sequence /clone=IMAGp998C11163; IMAGE:36364 /gb=BX101939 /gi=27831516 /ug=Hs.269499 /len=493	BX101939	Hs.269499	
7840	0.025072	UI-H-EI1-azh-n-13-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5848908 3', mRNA sequence /clone=IMAGE:5848908 /clone_end=3' /gb=BQ005547 /gi=19730447 /ug=Hs.445146 /len=994	BQ005547	Hs.445146	
7855	0.022485	EST(tz31e10.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2290218 3')	AI630897		NP_008993
7865	0.00344	hypothetical protein (clone ZC48G09)	AF086209		NP_056347
7888	0.034378	cDNA FLJ31107 fis, clone IMR322000152. /gb=AK055669 /gi=16550452 /ug=Hs.405954 /len=2250	AK055669	Hs.405954	
7896	0.042048	zh21a11.s1 Soares_pineal_gland_N3HPG cDNA clone IMAGE:412700 3', mRNA sequence /clone=IMAGE:412700 /clone_end=3' /gb=AA722220 /gi=2739927 /ug=Hs.290553 /len=342	AA722220	Hs.290553	
7899	0.004545	UI-E-DW0-agk-i-01-0-UI.r1 UI-E-DW0 cDNA clone UI-E-DW0-agk-i-01-0-UI 5', mRNA sequence /clone=UI-E-DW0-agk-i-01-0-UI /clone_end=5' /gb=BM696546 /gi=19009804 /ug=Hs.356149 /len=1200	BM696546	Hs.356149	
7900	0.034378	EST(hi90a11.x1 Soares_NFL_T_GBC_S1 clone IMAGE:2979548 3')	AW665382		
7908	0.04638	EST EST43399 Fetal brain I cDNA 3' end	AA338448		NP_112577
7912	0.031002	EST zx48b06.r1 Soares_testis_NHT cDNA clone IMAGE:795443 5' similar to contains Alu repetitive element;contains element MER13 repetitive element ;	AA454038		NP_060395
7928	0.005206	hypothetical protein HSPC195 (HSPC195), mRNA /cds=(293,889) /gb=NM_016463 /gi=20070365 /ug=Hs.356509 /len=1108	NM_016463	Hs.356509	



**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
7950	0.04638	cDNA sequence FLJ13553 fis, clone PLACE1007454	AK023615		NP_006818
7958	0.022485	enhancer of rudimentary (Drosophila) (ERH), mRNA /cds=(72,386) /gb=NM_004450 /gi=4758301 /ug=Hs.433413 /len=815	NM_004450	Hs.433413	NP_004441
7980	0.034378	splicing factor, arginine/serine-rich 12 (SFRS12), mRNA /cds=(342,1868) /gb=NM_139168 /gi=21040254 /ug=Hs.381165 /len=3811	NM_139168	Hs.381165	NP_631907
7981	0.046375	mRNA for KIAA1691 protein, partial cds. /cds=(78,1754) /gb=AB051478 /gi=20521967 /ug=Hs.94761 /len=4816	AB051478	Hs.94761	
7995	0.042048	lysophospholipase II (LYPLA2), mRNA /cds=(122,817) /gb=NM_007260 /gi=20302149 /ug=Hs.283655 /len=1648	NM_007260	Hs.283655	NP_009191
8004	0.038054	topoisomerase (DNA) I (TOP1), mRNA /cds=(247,2544) /gb=NM_003286 /gi=19913404 /ug=Hs.317 /len=3734	NM_003286	Hs.317	NP_003277
8019	0.038054	CGI-40 protein (CGI-40), mRNA /cds=(84,2621) /gb=NM_015996 /gi=7705756 /ug=Hs.33724 /len=3146	NM_015996	Hs.33724	NP_057080
8044	0.042048	chromosome 14 open reading frame 10 (C14orf10), mRNA /cds=(277,1638) /gb=NM_017917 /gi=8923599 /ug=Hs.49376 /len=1781	NM_017917	Hs.49376	NP_060387
8050	0.031002	hypothetical protein FLJ22557 (FLJ22557), mRNA /cds=(87,1001) /gb=NM_024713 /gi=13376012 /ug=Hs.106101 /len=2676	NM_024713	Hs.106101	NP_078989
8086	0.038054	transmembrane, prostate androgen induced RNA (TMEPAI), mRNA /cds=(321,1184) /gb=NM_020182 /gi=21361840 /ug=Hs.83883 /len=4839	NM_020182	Hs.83883	NP_064567
8112	0.034378	ankylosis, progressive (mouse) (ANKH), transcript variant 2, mRNA /cds=(265,1743) /gb=NM_054027 /gi=21536394 /ug=Hs.168640 /len=4031	NM_054027	Hs.168640	NP_473368
8176	0.020126	Similar to serine threonine protein kinase, clone MGC:20014 IMAGE:4554884, mRNA, complete cds (BC012085.1)	BC012085	Hs.8724	NP_009202

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8199	0.04638	hypothetical protein MGC18216 (MGC18216), mRNA /cds=(2207,2374) /gb=NM_152452 /gi=22748948 /ug=Hs.104679 /len=3270	NM_152452	Hs.104679	NP_689665
8212	0.00772	mRNA; cDNA DKFZp434D193 (from clone DKFZp434D193); partial cds /cds=(1,2240) /gb=AL080129 /gi=5262567 /ug=Hs.225841 /len=3605	AL080129	Hs.225841	
8222	0.022485	prefoldin 5 (PFDN5), transcript variant 1, mRNA /cds=(36,500) /gb=NM_002624 /gi=22202632 /ug=Hs.288856 /len=661	NM_002624	Hs.288856	NP_665904
8224	0.022485	hypothetical protein, MGC:7199 (LOC116150), mRNA /cds=(174,1055) /gb=NM_138459 /gi=20270242 /ug=Hs.289008 /len=2645	NM_138459	Hs.289008	NP_612468
8243	0.038054	T-cell lymphoma invasion and metastasis 2 (TIAM2), mRNA /cds=(51,3284) /gb=NM_012454 /gi=6912703 /ug=Hs.12598 /len=4586	NM_012454	Hs.12598	NP_036586
8316	0.038054	clone IMAGE:4794726, mRNA /gb=BC042028 /gi=27469506 /ug=Hs.367688 /len=1479	BC042028	Hs.367688	
8324	0.016031	hypothetical protein (FLJ10562 fis, clone NT2RP2002701)	AK001424		NP_057116
8338	0.031002	cDNA FLJ14181 fis, clone NT2RP2004300. /gb=AK024243 /gi=10436570 /ug=Hs.130874 /len=4411	AK024243	Hs.130874	
8358	0.027906	EST from cd34 stem cells Human sapiens cDNA clone CBCALE06	AF150123		
8363	0.031002	hypothetical protein FLJ14753 (FLJ14753), mRNA /cds=(247,1095) /gb=NM_032558 /gi=14211858 /ug=Hs.13453 /len=2593	NM_032558	Hs.13453	NP_115947
8366	0.04638	ob70e10.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:1336746 3', mRNA sequence /clone=IMAGE:1336746 /clone_end=3' /gb=AA809350 /gi=2878756 /ug=Hs.246180 /len=454	AA809350	Hs.246180	
8402	0.04638	EST (wh75b01.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2386537 3' similar to gb:X69392 60S RIBOSOMAL PROTEIN L26 (HUMAN);contains L1.b3 L1 repetitive element ;	A1809166		
8438	0.022485	mRNA sequence /gb=L26969 /gi=16905391 /ug=Hs.362852 /len=1738	L26969	Hs.362852	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8442	0.042048	UI-H-FL1-bgw-f-18-0-UI.s1 NCI_CGAP_FL1 cDNA clone UI-H-FL1-bgw-f-18-0-UI 3', mRNA sequence /clone=UI-H-FL1-bgw-f-18-0-UI /clone_end=3' /gb=BU634141 /gi=23301396 /ug=Hs.32163 /len=1068	BU634141	Hs.32163	
8443	0.031002	UI-H-EU1-bag-b-11-0-UI.s1 NCI_CGAP_Ct1 cDNA clone UI-H-EU1-bag-b-11-0-UI 3', mRNA sequence /clone=UI-H-EU1-bag-b-11-0-UI /clone_end=3' /gb=BQ448425 /gi=21251537 /ug=Hs.438826 /len=1023	BQ448425	Hs.438826	
8447	0.01798	cDNA FLJ32621 fis, clone STOMA2000395. /gb=AK057183 /gi=16552779 /ug=Hs.425445 /len=2648	AK057183	Hs.425445	
8462	0.044138	reverse transcriptase (non-exact)	AAB02291		
8473	0.022485	EST(xe97d09.x1 NCI_CGAP_Brn35 cDNA clone IMAGE:2616497 3')	AW129107		
8486	0.023403	cDNA, 3' end /clone=IMAGE:1935382 /clone_end=3' /gb=AI340092 /gi=4077019 /ug=Hs.327321 /len=361	AI340092	Hs.327321	NP_002370
8494	0.020126	UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059	BM994461	Hs.434057	
8511	0.01798	EST(yx64g06.r1 clone 266554 5')	N31192		
8523	0.01798	EST (ox48a03.x1 Soares_total_fetus_Nb2HF8_9w IMAGE:1659532 3')	AI038291		NP_612206
8528	0.009931	EST (602152342F1 NIH_MGC_81 cDNA clone IMAGE:4293442 5')	BF671599		
8531	0.042048	cDNA FLJ40915 fis, clone UTERU2005450. /gb=AK098234 /gi=21758205 /ug=Hs.207079 /len=2739	AK098234	Hs.207079	
8532	0.00789	sin3-associated polypeptide, 18kDa (SAP18), mRNA /cds=(65,526) /gb=NM_005870 /gi=23510407 /ug=Hs.23964 /len=2035	NM_005870	Hs.23964	NP_005861
8545	0.038054	as32a11.x1 Barstead aorta HPLRB6 cDNA clone IMAGE:2318876 3', mRNA sequence /clone=IMAGE:2318876 /clone_end=3' /gb=AI707688 /gi=4997464 /ug=Hs.369595 /len=518	AI707688	Hs.369595	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8560	0.04638	ribosomal protein L28 (RPL28), mRNA /cds=(43,456) /gb=NM_000991 /gi=13904865 /ug=Hs.356371 /len=500	NM_000991	Hs.356371	NP_000982
8561	0.004545	UI-H-BI2-agy-f-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2726158 3', mRNA sequence /clone=IMAGE:2726158 /clone_end=3' /gb=AW292315 /gi=6698951 /ug=Hs.435074 /len=1117	AW292315	Hs.435074	
8567	0.008979	UI-E-CL1-afg-f-16-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-afg-f-16-0-UI 5', mRNA sequence /clone=UI-E-CL1-afg-f-16-0-UI /clone_end=5' /gb=BM702572 /gi=19015830 /ug=Hs.446404 /len=1067	BM702572	Hs.446404	
8568	0.012669	EST(clone IMAGE:4733034 5' )	BG619661		
8572	0.038054	UI-H-EU0-azo-d-01-0-UI.s1 NCI_CGAP_Car1 cDNA clone IMAGE: 5851344 3', mRNA sequence /clone=IMAGE: 5851344 /clone_end=3' /gb=BQ180851 /gi=20356343 /ug=Hs.436432 /len=1067	BQ180851	Hs.436432	
8580	0.032415	BX096173 Soares_testis_NHT cDNA clone IMAGp998F151793, mRNA sequence /clone=IMAGp998F151793 ; IMAGE:7 30766 /gb=BX096173 /gi=27842669 /ug=Hs.188780 /len=556	BX096173	Hs.188780	
8595	0.027906	ribosomal protein L3 (RPL3), mRNA /cds=(27,1238) /gb=NM_000967 /gi=16507968 /ug=Hs.119598 /len=1311	NM_000967	Hs.119598	NP_000958
8596	0.008765	UI-E-CQ1-acq-f-05-0-UI.r1 UI-E-CQ1 cDNA clone UI-E-CQ1-acq-f-05-0-UI 5', mRNA sequence /clone=UI-E-CQ1-acq-f-05-0-UI /clone_end=5' /gb=BM688680 /gi=19001938 /ug=Hs.406520 /len=934	BM688680	Hs.406520	
8597	0.022485	hypothetical protein MGC23918 (MGC23918), mRNA /cds=(17,517) /gb=NM_144716 /gi=21389496 /ug=Hs.43773 /len=874	NM_144716	Hs.43773	NP_653317
8613	0.006784	ESTs, cDNA, 3' end /clone=IMAGE:1658128 /clone_end=3' /gb=AI039268 /gi=3278462 /ug=Hs.131973 /len=437	AI039268	Hs.131973	
8618	0.031002	EST(HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA )	BG896206		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8669	0.04638	cDNA FLJ10190 fis, clone HEMBA1004753. /gb=AK001052 /gi=7022081 /ug=Hs.274546 /len=1318	AK001052	Hs.274546	
8670	0.006049	mRNA; cDNA DKFZp434A128 (from clone DKFZp434A128); partial cds /cds=(621,2888) /gb=AL122120 /gi=6102946 /ug=Hs.313948 /len=4493	AL122120	Hs.313948	
8675	0.04638	UI-H-EI0-ayo-a-20-0-UI.s1 NCI_CGAP_EI0 cDNA clone IMAGE:5841307 3', mRNA sequence /clone=IMAGE:5841307 /clone_end=3' /gb=BQ004581 /gi=19729481 /ug=Hs.412459 /len=1095	BQ004581	Hs.412459	
8729	0.020126	cDNA FLJ30135 fis, clone BRACE2000061. /gb=AK054697 /gi=16549295 /ug=Hs.34906 /len=2024	AK054697	Hs.34906	NP_776170
8732	0.011228	UI-H-DT1-awm-l-24-0-UI.s1 NCI_CGAP_DT1 cDNA clone IMAGE:5891495 3', mRNA sequence /clone=IMAGE:5891495 /clone_end=3' /gb=BQ019127 /gi=19754404 /ug=Hs.434910 /len=896	BQ019127	Hs.434910	
8769	0.042048	EST(adult brain Danio rerio cDNA clone 4966301 5' similar to SW:RLA1_CHICK P18660 60S ACIDIC RIBOSOMAL PROTEIN P1. ;contains element MER22 repetitive element ; )	BI429083		
8782	0.025072	mitochondrion, complete genome	NC_001807		
8791	0.016031	tg51b06.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2112275 3', mRNA sequence /clone=IMAGE:2112275 /clone_end=3' /gb=AI419722 /gi=4265653 /ug=Hs.161220 /len=484	AI419722	Hs.161220	
8792	0.038054	EST(cDNA clone IMAGE:2092653 3' )	AI381556		
8796	0.020126	ESTs, cDNA, 3' end /clone=UI-E-EJ0-aii-l-19-0-UI /clone_end=3' /gb=BM681301 /gi=18991197 /ug=Hs.355029 /len=591	BM681301	Hs.355029	
8808	0.014265	EST(cDNA clone CS0DF021YG07 5 prime )	AL535948		NP_006612
8836	0.027906	No significant match	SEQ.ID.No.33		
8856	0.01798	control			
8874	0.009931	No significant match (ORF:+1:256~491[237])	SEQ.ID.No.26		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
8889	0.020912	No significant match (ORF:+2:50~238[189], +3:90~245[156])	SEQ.ID.No.65		
8906	0.042048	apoptosis, caspase activation inhibitor (AVEN), mRNA /cds=(53,1141) /gb=NM_020371 /gi=9966840 /ug=Hs.63168 /len=1549	NM_020371	Hs.63168	NP_065104
8939	0.034378	hypothetical protein GL009 (GL009), mRNA /cds=(78,629) /gb=NM_032492 /gi=14210501 /ug=Hs.24054 /len=1097	NM_032492	Hs.24054	NP_115881
8968	0.038054	xc57a09.x1 NCI_CGAP_Eso2 cDNA clone IMAGE:2588344 3' similar to contains Alu repetitive element;, mRNA sequence /clone=IMAGE:2588344 /clone_end=3' /gb=AW084739 /gi=6039891 /ug=Hs.445134 /len=509	AW084739	Hs.445134	
8969	0.016031	EST(AV730379 HTF cDNA clone HTFAAA05 5')	AV730379		
8970	0.005206	on43h10.y5 NCI_CGAP_Co8 cDNA clone IMAGE:1559491 5', mRNA sequence /clone=IMAGE:1559491 /clone_end=5' /gb=AI793153 /gi=5340869 /ug=Hs.58262 /len=521	AI793153	Hs.58262	
8980	0.008765	EST yq55e03.r1 Soares fetal liver spleen 1NFLS H.sapiens cDNA clone IMAGE:199708 5' similar to contains Alu repetitive element;	R96686		
9003	0.016031	hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA /cds=(514,1290) /gb=NM_031284 /gi=21361960 /ug=Hs.10748 /len=2262	NM_031284	Hs.10748	NP_112574
9006	0.04638	cDNA FLJ38383 fis, clone FEBRA2003726. /gb=AK095702 /gi=21755022 /ug=Hs.433517 /len=3240	AK095702	Hs.433517	
9017	0.006784	UI-H-FH1-bfk-m-06-0-UI.s1 NCI_CGAP_FH1 cDNA clone UI-H-FH1-bfk-m-06-0-UI 3', mRNA sequence /clone=UI-H-FH1-bfk-m-06-0-UI /clone_end=3' /gb=BU618627 /gi=23284842 /ug=Hs.192435 /len=1099	BU618627	Hs.192435	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9041	0.005949	7l40g01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3524136 3', mRNA sequence /clone=IMAGE:3524136 /clone_end=3' /gb=BF112131 /gi=10941821 /ug=Hs.288083 /len=620	BF112131	Hs.288083	
9042	0.04638	UI-CF-FN0-aeu-b-13-0-UI.s1 UI-CF- FN0 cDNA clone UI-CF-FN0-aeu-b-13-0- UI 3', mRNA sequence /clone=UI-CF- FN0-aeu-b-13-0-UI /clone_end=3' /gb=BU689604 /gi=23547505 /ug=Hs.273830 /len=1066	BU689604	Hs.273830	
9043	0.038054	CocoaCrisp (LOC83690), mRNA /cds=(376,1878) /gb=NM_031461 /gi=21314740 /ug=Hs.182364 /len=2962	NM_031461	Hs.182364	NP_113649
9046	0.00772	EST(xa08a12.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2567710 3')	AW074833		
9055	0.034378	zi76d12.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:436727 3', mRNA sequence /clone=IMAGE:436727 /clone_end=3' /gb=AA702930 /gi=2706043 /ug=Hs.189679 /len=478	AA702930	Hs.189679	
9063	0.042048	clone 23612 mRNA sequence /gb=U90902 /gi=1913880 /ug=Hs.82141 /len=1548	U90902	Hs.82141	
9078	0.031002	cDNA FLJ13207 fis, clone NT2RP4000023. /gb=AK023269 /gi=10435128 /ug=Hs.14355 /len=2633	AK023269	Hs.14355	
9110	0.04638	UI-E-CR1-adz-a-04-0-UI.r1 UI-E-CR1 cDNA clone UI-E-CR1-adz-a-04-0-UI 5', mRNA sequence /clone=UI-E-CR1-adz- a-04-0-UI /clone_end=5' /gb=BM706524 /gi=19019782 /ug=Hs.421063 /len=1149	BM706524	Hs.421063	
9112	0.04638	UI-1-BC1-ajs-e-06-0-UI.s1 NCI_CGAP_PI2 cDNA clone UI-1-BC1- ajs-e-06-0-UI 3', mRNA sequence /clone=UI-1-BC1-ajs-e-06-0-UI /clone_end=3' /gb=BQ010796 /gi=19735697 /ug=Hs.120770 /len=904	BQ010796	Hs.120770	
9114	0.012669	EST(cDNA clone IMAGE:2504565 3')	AW009489		
9129	0.034378	EST(cDNA.	AW896077		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9150	0.031002	EST, cDNA, 3' end /clone=IMAGE:3214604 /clone_end=3' /gb=BE503107 /gi=9705515 /ug=Hs.281951 /len=368	BE503107	Hs.281951	
9154	0.042048	mRNA; cDNA DKFZp564B213 (from clone DKFZp564B213) /gb=AL049240 /gi=4499973 /ug=Hs.380268 /len=767	AL049240	Hs.380268	
9157	0.031002	mRNA; cDNA DKFZp451O1818 (from clone DKFZp451O1818) /gb=AL832650 /gi=21733226 /ug=Hs.12396 /len=4870	AL832650	Hs.12396	
9243	0.04638	AV700621 GKC cDNA clone GKCDKF09 3', mRNA sequence /clone=GKCDKF09 /clone_end=3' /gb=AV700621 /gi=10302592 /ug=Hs.191445 /len=809	AV700621	Hs.191445	
9253	0.022485	603390782F1 NIH_MGC_87 cDNA clone IMAGE:5399756 5', mRNA sequence /clone=IMAGE:5399756 /clone_end=5' /gb=BI860842 /gi=16001577 /ug=Hs.112472 /len=917	BI860842	Hs.112472	
9319	0.011228	No significant match (ORF:+2:2~226[225]), low complexity	SEQ.ID.No.17		
9387	0.038054	RAB35, member RAS oncogene family (RAB35), mRNA /cds=(117,722) /gb=NM_006861 /gi=19923377 /ug=Hs.94308 /len=2887	NM_006861	Hs.94308	NP_006852
9424	0.014265	MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds	U63630		
9426	0.048742	clone IMAGE:4130494, mRNA /gb=BC023543 /gi=23270740 /ug=Hs.112844 /len=4567	BC023543	Hs.112844	
9450	0.016031	FK506 binding protein 3, 25kDa (FKBP3), mRNA /cds=(412,1086) /gb=NM_002013 /gi=17149845 /ug=Hs.379557 /len=1420	NM_002013	Hs.379557	NP_002004
9453	0.006784	mRNA for KIAA1705 protein, partial cds. /cds=(1714,3210) /gb=AB051492 /gi=12697954 /ug=Hs.7076 /len=3949	AB051492	Hs.7076	
9463	0.022485	tropomyosin 3 (TPM3), mRNA /cds=(52,798) /gb=NM_153649 /gi=24119202 /ug=Hs.85844 /len=2089	NM_153649	Hs.85844	NP_705935
9488	0.004545	UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1), mRNA /cds=(312,1829) /gb=NM_003115 /gi=19923738 /ug=Hs.21293 /len=2332	NM_003115	Hs.21293	NP_003106



TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9491	0.025072	clone IMAGE:2960008, mRNA /gb=BC017253 /gi=16878090 /ug=Hs.433345 /len=1405	BC017253	Hs.433345	
9548	0.027906	ubiquitin specific protease 1 (USP1), mRNA /cds=(246,2603) /gb=NM_003368 /gi=21361109 /ug=Hs.35086 /len=3379	NM_003368	Hs.35086	NP_003359
9553	0.04638	protein phosphatase 1, catalytic subunit, beta isoform (PPP1CB), mRNA /cds=(259,1242) /gb=NM_002709 /gi=4506004 /ug=Hs.21537 /len=3590	NM_002709	Hs.21537	NP_002700
9576	0.01798	collagen, type XV, alpha 1 (COL15A1), mRNA /cds=(166,4332) /gb=NM_001855 /gi=18641349 /ug=Hs.83164 /len=5222	NM_001855	Hs.83164	NP_001846
9586	0.020126	NRRL 4123 mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence	U29233		
9594	0.01798	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 2 (SERPINE2), mRNA /cds=(210,1406) /gb=NM_006216 /gi=24307906 /ug=Hs.21858 /len=2129	NM_006216	Hs.21858	NP_006207
9610	0.012669	nuclear DNA-binding protein (C1D), transcript variant 1, mRNA /cds=(64,489) /gb=NM_006333 /gi=27894371 /ug=Hs.15164 /len=1200	NM_006333	Hs.15164	NP_775269
9612	0.04638	ubiquitin-conjugating enzyme E2G 1 (UBC7 C. elegans) (UBE2G1), mRNA /cds=(167,679) /gb=NM_003342 /gi=21314607 /ug=Hs.78563 /len=2430	NM_003342	Hs.78563	NP_003333
9629	0.04638	vaccinia related kinase 1 (VRK1), mRNA /cds=(76,1266) /gb=NM_003384 /gi=4507902 /ug=Hs.422789 /len=1662	NM_003384	Hs.422789	NP_003375
9669	0.048742	hypothetical protein(FLJ20378)	BAA91131		
9693	0.016031	hypothetical protein LOC93380 (LOC93380), mRNA /cds=(301,696) /gb=NM_173470 /gi=27735036 /ug=Hs.110702 /len=3704	NM_173470	Hs.110702	NP_775741
9699	0.025072	EST(zeh1487.seq.F Zebrafish Embryonic Heart cDNA Library cDNA 5')	AI354098		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9701	0.034378	DKFZP586G1517 protein (DKFZP586G1517), mRNA /cds=(127,2328) /gb=NM_015440 /gi=24308062 /ug=Hs.44155 /len=2749	NM_015440	Hs.44155	NP_056255
9716	0.00772	EST(EST23220 Adipose tissue, white II 5' contains Alu repeat)	AA320820		
9724	0.027906	hypothetical protein BC012010 (LOC113174), mRNA /cds=(30,1457) /gb=NM_138421 /gi=19923942 /ug=Hs.183733 /len=1527	NM_138421	Hs.183733	NP_612430
9740	0.016031	periphilin 1 (PPHLN1), mRNA /cds=(94,1197) /gb=NM_016488 /gi=21361573 /ug=Hs.281428 /len=1643	NM_016488	Hs.281428	NP_057572
9747	0.022485	EST(ya49e04.r2 clone 53081 5')	R16260		
9761	0.04638	hypothetical protein FLJ22557 (FLJ22557), mRNA /cds=(87,1001) /gb=NM_024713 /gi=13376012 /ug=Hs.106101 /len=2676	NM_024713	Hs.106101	NP_078989
9804	0.038054	RNA polymerase III subunit RPC2 (RPC2), mRNA /cds=(54,3455) /gb=NM_018082 /gi=24475856 /ug=Hs.197642 /len=4102	NM_018082	Hs.197642	NP_060552
9805	0.025072	EST (qh12h02.x1 Soares_NFL_T_GBC_S1 IMAGE:1844499 3')	AI240516		
9819	0.025072	EST (yq42a05.r1 Soares fetal liver spleen)	R94397		
9840	0.022485	hypothetical protein FLJ20244 (FLJ20244), mRNA /cds=(89,2068) /gb=NM_017722 /gi=8923218 /ug=Hs.158947 /len=2137	NM_017722	Hs.158947	NP_060192
9850	0.020126	cDNA FLJ11946 fis, clone HEMBB1000709. /gb=AK022008 /gi=10433321 /ug=Hs.323231 /len=3241	AK022008	Hs.323231	
9875	0.004545	heat shock 27kDa protein 2 (HSPB2), mRNA /cds=(70,618) /gb=NM_001541 /gi=4504518 /ug=Hs.78846 /len=874	NM_001541	Hs.78846	NP_001532
9903	0.00772	hypothetical protein MGC40157 (MGC40157), mRNA /cds=(106,498) /gb=NM_152350 /gi=22748758 /ug=Hs.295362 /len=1250	NM_152350	Hs.295362	NP_689563
9904	0.014265	O-linked mannose beta1,2-N-acetylglucosaminyltransferase (FLJ20277), mRNA /cds=(142,2124) /gb=NM_017739 /gi=8923252 /ug=Hs.183860 /len=2737	NM_017739	Hs.183860	NP_060209

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
9919	0.025072	B-cell receptor-associated protein BAP29 (BAP29), mRNA /cds=(47,775) /gb=NM_018844 /gi=9994198 /ug=Hs.27135 /len=1085	NM_018844	Hs.27135	NP_061332
9936	0.038054	x 009 protein (MDS009), mRNA /cds=(127,534) /gb=NM_020234 /gi=9910425 /ug=Hs.64641 /len=1133	NM_020234	Hs.64641	NP_064619
9946	0.025072	mitogen-activated protein kinase kinase 1 (MAP2K1), mRNA /cds=(73,1254) /gb=NM_002755 /gi=14589898 /ug=Hs.3446 /len=2222	NM_002755	Hs.3446	NP_002746
10015	0.034378	mRNA for KIAA1228 protein, partial cds. /cds=(1,2534) /gb=AB033054 /gi=20521803 /ug=Hs.306867 /len=5742	AB033054	Hs.306867	
10016	0.031002	glycosyltransferase (LOC83468), mRNA /cds=(408,1457) /gb=NM_031302 /gi=21314737 /ug=Hs.159993 /len=1908	NM_031302	Hs.159993	NP_112592
10019	0.038054	serologically defined colon cancer antigen 33 (SDCCAG33), mRNA /cds=(295,2358) /gb=NM_005786 /gi=15451922 /ug=Hs.284217 /len=2858	NM_005786	Hs.284217	NP_005777
10025	0.002982	SPARC related modular calcium binding 2 (SMOC2), mRNA /cds=(21,1394) /gb=NM_022138 /gi=24308276 /ug=Hs.22209 /len=2947	NM_022138	Hs.22209	NP_071421
10060	0.014265	roundabout, axon guidance receptor, 1 (Drosophila) (ROBO1), transcript variant 2, mRNA /cds=(964,5802) /gb=NM_133631 /gi=19743805 /ug=Hs.301198 /len=7475	NM_133631	Hs.301198	NP_598334
10084	0.012669	hypothetical protein MGC11034 (MGC11034), mRNA /cds=(246,641) /gb=NM_031453 /gi=13899290 /ug=Hs.103378 /len=3301	NM_031453	Hs.103378	NP_113641
10102	0.04638	hypothetical protein FLJ23445 (FLJ23445), mRNA /cds=(44,658) /gb=NM_025075 /gi=13376622 /ug=Hs.288151 /len=963	NM_025075	Hs.288151	NP_079351
10130	0.014741	UI-H-EU1-bad-c-14-0-UI.s1 NCI_CGAP_Ct1 cDNA clone UI-H-EU1-bad-c-14-0-UI 3', mRNA sequence /clone=UI-H-EU1-bad-c-14-0-UI /clone_end=3' /gb=BQ447141 /gi=21250253 /ug=Hs.445111 /len=1032	BQ447141	Hs.445111	

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10167	0.034378	EST(zs29d10.r1 NCI_CGAP_GCB1 IMAGE:686611 5') short match	AA255979		NP_004828
10178	0.011228	EST382135 MAGE resequences, MAGK cDNA, mRNA sequence /gb=AW970055 /gi=8159900 /ug=Hs.324815 /len=764	AW970055	Hs.324815	
10191	0.031002	EST(HSPD24973 HM3 clone s3000036E04)	F32327		
10215	0.012669	UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667	BM727413	Hs.112619	
10228	0.00772	hypothetical protein FLJ10342 (FLJ10342), mRNA /cds=(534,1145) /gb=NM_018064 /gi=14149717 /ug=Hs.101514 /len=1506	NM_018064	Hs.101514	NP_060534
10290	0.031002	ox21f03.x1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:1656989 3', mRNA sequence /clone=IMAGE:1656989 /clone_end=3' /gb=AI038379 /gi=3277573 /ug=Hs.131865 /len=516	AI038379	Hs.131865	
10312	0.026138	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa (TAF1A), transcript variant 1, mRNA /cds=(190,1542) /gb=NM_005681 /gi=21536363 /ug=Hs.153088 /len=1893	NM_005681	Hs.153088	NP_647603
10316	0.022485	clone IMAGE:5295896, mRNA /gb=BC043240 /gi=27695834 /ug=Hs.104413 /len=2136	BC043240	Hs.104413	
10323	0.022485	mRNA; cDNA DKFZp434K1115 (from clone DKFZp434K1115); complete cds /cds=(97,2877) /gb=AL136764 /gi=12053044 /ug=Hs.42676 /len=4868	AL136764	Hs.42676	
10350	0.038054	hypothetical protein FLJ90013 (FLJ90013), mRNA /cds=(15,1703) /gb=NM_153365 /gi=23503310 /ug=Hs.25119 /len=3382	NM_153365	Hs.25119	NP_699196
10364	0.027906	EST (QV3-NN1023-130500-178-g10 NN1023)	AW902437		
10380	0.016031	Hypothetical protein(cDNA: FLJ22479 fis, clone HRC10831)	AK026132		NP_079176
10401	0.038054	EST (Clontech human aorta polyA mRNA (#6572) cDNA clone GEN-041E02 5')	C14262		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10423	0.04638	muscleblind-like protein MBLL39 (MBLL39), transcript variant 1, mRNA /cds=(782,1885) /gb=NM_144778 /gi=21464124 /ug=Hs.283609 /len=4665	NM_144778	Hs.283609	NP_659002
10429	0.020126	binder of Rho GTPase 3-like (MGC21945), mRNA /cds=(340,786) /gb=NM_145057 /gi=21450817 /ug=Hs.352987 /len=929	NM_145057	Hs.352987	NP_659494
10437	0.038054	UI-H-EI1-aze-c-02-0-UI.s1 NCI_CGAP_EI1 cDNA clone IMAGE:5847481 3', mRNA sequence /clone=IMAGE:5847481 /clone_end=3' /gb=BQ003590 /gi=19728490 /ug=Hs.29698 /len=1051	BQ003590	Hs.29698	
10439	0.027906	clone IMAGE:4157625, mRNA /gb=BC033767 /gi=22832873 /ug=Hs.271450 /len=1515	BC033767	Hs.271450	
10454	0.038054	EST(tm27f02.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2157819 3')	AI479365		
10475	0.025072	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1 (SLC25A1), mRNA /cds=(100,1035) /gb=NM_005984 /gi=21389314 /ug=Hs.111024 /len=1619	NM_005984	Hs.111024	NP_005975
10496	0.027906	zh69e06.s1 Soares_fetal_liver_spleen_1NFLS_S1 cDNA clone IMAGE:417346 3', mRNA sequence /clone=IMAGE:417346 /clone_end=3' /gb=W89192 /gi=1404504 /ug=Hs.194238 /len=471	W89192	Hs.194238	
10501	0.038054	UI-E-DW0-agg-d-24-0-UI.r1 UI-E-DW0 cDNA clone UI-E-DW0-agg-d-24-0-UI 5', mRNA sequence /clone=UI-E-DW0-agg-d-24-0-UI /clone_end=5' /gb=BM706154 /gi=19019412 /ug=Hs.433446 /len=1003	BM706154	Hs.433446	
10502	0.006784	EST(cDNA clone IMAGE:4944078 5')	BG913252		NP_775882
10503	0.016031	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
10506	0.005206	K-EST0187941 L14ChoiCK0 cDNA clone L14ChoiCK0-30-C05 5', mRNA sequence /clone=L14ChoiCK0-30-C05 /clone_end=5' /gb=CB135678 /gi=28102621 /ug=Hs.435110 /len=419	CB135678	Hs.435110	
10512	0.016031	POLY A			

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10531	0.04638	mRNA; cDNA DKFZp686J172 (from clone DKFZp686J172) /gb=AL832206 /gi=21732751 /ug=Hs.56896 /len=6055	AL832206	Hs.56896	
10539	0.038054	ribosomal protein, large, P1 (RPLP1), mRNA /cds=(130,474) /gb=NM_001003 /gi=16905511 /ug=Hs.424299 /len=512	NM_001003	Hs.424299	NP_000994
10540	0.004545	BX116063 NCI_CGAP_Brn23 cDNA clone IMAGp998O244959, mRNA sequence /clone=IMAGp998O244959;_IMAGE:2016239 /gb=BX116063 /gi=27839769 /ug=Hs.127872 /len=537	BX116063	Hs.127872	
10546	0.031002	cDNA FLJ13585 fis, clone PLACE1009150. /gb=AK023647 /gi=10435632 /ug=Hs.43047 /len=3430	AK023647	Hs.43047	
10561	0.014265	wn03h10.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2444419 3', mRNA sequence /clone=IMAGE:2444419 /clone_end=3' /gb=AI924266 /gi=5660230 /ug=Hs.370113 /len=514	AI924266	Hs.370113	
10566	0.008765	actin, beta (ACTB), mRNA /cds=(74,1201) /gb=NM_001101 /gi=5016088 /ug=Hs.426930 /len=1793	NM_001101	Hs.426930	NP_001092
10570	0.031002	thymosin, beta 4, X chromosome (TMSB4X), mRNA /cds=(78,212) /gb=NM_021109 /gi=11056060 /ug=Hs.75968 /len=556	NM_021109	Hs.75968	NP_066932
10578	0.025072	xj80g04.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2663574 3', mRNA sequence /clone=IMAGE:2663574 /clone_end=3' /gb=AW172661 /gi=6438609 /ug=Hs.257251 /len=451	AW172661	Hs.257251	
10610	0.025072	cDNA, 3' end /clone=IMAGE:3476408 /clone_end=3' /gb=BF058813 /gi=10812709 /ug=Hs.319312 /len=382	BF058813	Hs.319312	NP_001454
10673	0.042048	mitochondrial ribosomal protein S18C (MRPS18C), nuclear gene encoding mitochondrial protein, mRNA /cds=(60,488) /gb=NM_016067 /gi=7705629 /ug=Hs.3385 /len=1014	NM_016067	Hs.3385	NP_057151
10683	0.014265	EST388886 MAGE resequences, MAGO cDNA, mRNA sequence /gb=AW976777 /gi=8168011 /ug=Hs.223578 /len=519	AW976777	Hs.223578	

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10684	0.034378	EST(cDNA clone IMAGE:4090855 3' )	BF447403		NP_002806
10710	0.025072	No significant match	SEQ.ID.No.46		
10717	.0.04638	No significant match	SEQ.ID.No.83		
10773	0.006784	EST (RC3-CT0254-300800-022-g07 CT0254)	BE927223		
10779	0.034378	EST (ADB cDNA clone ADBAKA02 5')	AV704531		
10790	0.016031	similar to zinc finger protein 22 (KOX 15) (LOC166793), mRNA /cds=(1401,2147) /gb=NM_145291 /gi=21686968 /ug=Hs.94013 /len=2634	NM_145291	Hs.94013	NP_660334
10805	0.031002	EST(ak84d11.s1 Barstead spleen HPLRB2 cDNA clone IMAGE:1414581 3' similar to contains MER10.t3 MER10 repetitive element)	AA845289		
10806	0.016031	EST (qj86f09.x1 NCI_CGAP_Kid3 cDNA clone IMAGE:1866377 3' similar to contains MER30.t3 MER30 repetitive element )	AI244320		
10807	0.042048	methyltransferase like 3 (METTL3), mRNA /cds=(87,1829) /gb=NM_019852 /gi=21361826 /ug=Hs.268149 /len=1959	NM_019852	Hs.268149	NP_062826
10811	0.025072	EST from clone 208499, full insert /gb=AL355688 /gi=7799136 /ug=Hs.6655 /len=1831	AL355688	Hs.6655	
10839	0.00772	calcium binding protein Cab45 precursor (Cab45), mRNA /cds=(294,1340) /gb=NM_016547 /gi=7706572 /ug=Hs.42806 /len=2092	NM_016547	Hs.42806	NP_057631
10841	0.01798	zinc finger protein 306 (ZNF306), mRNA /cds=(149,1765) /gb=NM_024493 /gi=24308296 /ug=Hs.66774 /len=2242	NM_024493	Hs.66774	NP_077819
10867	0.022485	7k59b12.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3479758 3', mRNA sequence /clone=IMAGE:3479758 /clone_end=3' /gb=BF059412 /gi=10813230 /ug=Hs.319320 /len=453	BF059412	Hs.319320	
10894	0.042048	C1q and tumor necrosis factor related protein 3 (C1QTNF3), mRNA /cds=(84,824) /gb=NM_030945 /gi=13569918 /ug=Hs.171929 /len=1710	NM_030945	Hs.171929	NP_852100
10910	0.042048	EST (tg92b06.x1 NCI_CGAP_CLL1 cDNA clone IMAGE:2116211 3' similar to contains Alu repetitive element;)	AI401289		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
10917	0.022485	activated RNA polymerase II transcription cofactor 4 (PC4), mRNA /cds=(57,440) /gb=NM_006713 /gi=19923783 /ug=Hs.349506 /len=1336	NM_006713	Hs.349506	NP_006704
10930	0.031002	Similar to RIKEN cDNA 2810004N23 gene, clone MGC:46269 IMAGE:5589128, mRNA, complete cds /cds=(57,905) /gb=BC036800 /gi=22477333 /ug=Hs.390881 /len=1468	BC036800	Hs.390881	
10942	0.04638	EST(ze42c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361642 5' )	W96264		
10946	0.031002	of yeast long chain polyunsaturated fatty acid elongation enzyme 2 (HELO1), mRNA /cds=(345,1244) /gb=NM_021814 /gi=21361903 /ug=Hs.250175 /len=3011	NM_021814	Hs.250175	NP_068586
10949	0.022485	yo73e02.s1 Soares breast 3NbHBst cDNA clone IMAGE:183578 3', mRNA sequence /clone=IMAGE:183578 /clone_end=3' /gb=H44042 /gi=920094 /ug=Hs.391565 /len=417	H44042	Hs.391565	
10958	0.011228	FLJ30424 fis, clone BRACE2008881, weakly similar to ZINC FINGER PROTEIN 195 /cds=UNKNOWN /gb=AK054986 /gi=16549625 /ug=Hs.21423 /len=2144	AK054986	Hs.21423	
10989	0.04638	BX102645 NCI_CGAP_Brn23 cDNA clone IMAGp998L144327, mRNA sequence /clone=IMAGp998L144327; IMAGE:1703965 /gb=BX102645 /gi=27831887 /ug=Hs.146883 /len=786	BX102645	Hs.146883	
11006	0.005206	ab12g02.s1 Stratagene lung (#937210) cDNA clone IMAGE:840626 3', mRNA sequence /clone=IMAGE:840626 /clone_end=3' /gb=AA487969 /gi=2215400 /ug=Hs.96692 /len=466	AA487969	Hs.96692	
11020	0.025072	UI-H-DH0-aui-j-10-0-UI.s1 NCI_CGAP_DH0 cDNA clone IMAGE:5871081 3', mRNA sequence /clone=IMAGE:5871081 /clone_end=3' /gb=BM994461 /gi=19719362 /ug=Hs.434057 /len=2059	BM994461	Hs.434057	
11027	0.034378	cDNA FLJ12885 fis, clone NT2RP2003988. /gb=AK022947 /gi=10434630 /ug=Hs.36093 /len=2000	AK022947	Hs.36093	



TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11030	0.022485	ESTs, cDNA, 3' end /clone=IMAGE:2308223 /clone_end=3' /gb=AI671885 /gi=4851616 /ug=Hs.110855 /len=593	AI671885	Hs.110855	
11032	0.029136	nj38c05.s1 NCI_CGAP_AA1 cDNA clone IMAGE:994760 3' similar to gb:M62424 THROMBIN RECEPTOR PRECURSOR mRNA sequence /clone=IMAGE:994760 /clone_end=3' /gb=AA548630 /gi=2318912 /ug=Hs.105848 /len=555	AA548630	Hs.105848	
11033	0.016031	FLJ30661 fis, clone DFNES2000526 /cds=UNKNOWN /gb=AK055223 /gi=16549904 /ug=Hs.265540 /len=2514	AK055223	Hs.265540	NP_057178
11044	0.034378	EST(fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:241467 3' )	H90418		
11055	0.038054	UI-E-CL1-aez-f-02-0-UI.r1 UI-E-CL1 cDNA clone UI-E-CL1-aez-f-02-0-UI 5', mRNA sequence /clone=UI-E-CL1-aez-f- 02-0-UI /clone_end=5' /gb=BM695854 /gi=19009112 /ug=Hs.21509 /len=1260	BM695854	Hs.21509	
11056	0.01798	cDNA: FLJ22050 fis, clone HEP09454. /gb=AK025703 /gi=10438305 /ug=Hs.173705 /len=1990	AK025703	Hs.173705	
11067	0.029136	ESTs, cDNA, 5' end /clone=IMAGE:4474821 /clone_end=5' /gb=BG253800 /gi=12763616 /ug=Hs.128894 /len=950	BG253800	Hs.128894	NP_524576
11068	0.031002	mRNA; cDNA DKFZp586G1520 (from clone DKFZp586G1520) /gb=AL050148 /gi=4884359 /ug=Hs.31834 /len=3030	AL050148	Hs.31834	
11069	0.00772	ESTs, Stratagene ovarian cancer (#937219 cDNA clone IMAGE:595374 3' similar to TR:Q13129 Q13129 ZN-15 RELATED ZINC FINGER PROTEIN ;	AI732587		
11091	0.042048	BX091936 Soares placenta Nb2HP cDNA clone IMAGp998N02193 ; IMAGE:135745, mRNA sequence /clone=IMAGp998N02193 ;_IMAGE:13 5745 /gb=BX091936 /gi=27822661 /ug=Hs.24598 /len=688	BX091936	Hs.24598	
11110	0.020126	cDNA FLJ37125 fis, clone BRACE2022638. /gb=AK094444 /gi=21753507 /ug=Hs.12030 /len=2720	AK094444	Hs.12030	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11118	0.025072	BX100041 Soares pineal gland 3NbHPG cDNA clone IMAGp998D02466, mRNA sequence /clone=IMAGp998D02466_/_IMAGE:23 1505 /gb=BX100041 /gi=27830398 /ug=Hs.446061 /len=718	BX100041	Hs.446061	
11166	0.010197	ym53e05.s1 Soares infant brain 1NIB cDNA clone IMAGE:51803 3', mRNA sequence /clone=IMAGE:51803 /clone_end=3' /gb=H24464 /gi=893159 /ug=Hs.417814 /len=487	H24464	Hs.417814	
11168	0.042048	hv66b12.x1 NCI_CGAP_Lu24 cDNA clone IMAGE:3178367 3', mRNA sequence /clone=IMAGE:3178367 /clone_end=3' /gb=BE220031 /gi=8907349 /ug=Hs.192491 /len=379	BE220031	Hs.192491	
11193	0.038054	control			
11198	0.013065	cDNA FLJ23679 fis, clone HEP09084. /gb=AK074259 /gi=18676812 /ug=Hs.351597 /len=2006	AK074259	Hs.351597	
11200	0.04638	EST(cDNA clone IMAGE:3087494 3')	BF509784		
11224	0.034378	No significant match	SEQ.ID.No.93		
11238	0.027906	nebulin mRNA, partial cds. /gb=U35637 /gi=1205988 /ug=Hs.83870 /len=9443	U35637	Hs.83870	NP_004534
11257	0.04638	mRNA for FLJ00086 protein, partial cds. /cds=(1951,3150) /gb=AK024487 /gi=10440487 /ug=Hs.343828 /len=4456	AK024487	Hs.343828	NP_835461
11261	0.009931	hypothetical protein MGC14480 (MGC14480), mRNA /cds=(18,209) /gb=NM_144998 /gi=21450710 /ug=Hs.37616 /len=844	NM_144998	Hs.37616	NP_659435
11263	0.027906	KIAA1804 protein, partial cds /cds=UNKNOWN /gb=AB058707 /gi=14017824 /ug=Hs.50883	AB058707	Hs.50883	NP_115811
11297	0.022485	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) (FDPS), mRNA /cds=(115,1374) /gb=NM_002004 /gi=4503684 /ug=Hs.335918 /len=1430	NM_002004	Hs.335918	NP_001995
11313	0.027459	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa (NDUFA1), nuclear gene encoding mitochondrial protein, mRNA /cds=(143,355) /gb=NM_004541 /gi=13699820 /ug=Hs.74823 /len=479	NM_004541	Hs.74823	NP_004532

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11324	0.01798	endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1 (HERPUD1), mRNA /cds=(96,1271) /gb=NM_014685 /gi=7661869 /ug=Hs.146393 /len=1884	NM_014685	Hs.146393	NP_055500
11325	0.027906	tetratricopeptide repeat domain 8 (TTC8), mRNA /cds=(53,1648) /gb=NM_144596 /gi=21389382 /ug=Hs.55158 /len=2241	NM_144596	Hs.55158	NP_653197
11335	0.020126	COX11 cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA /cds=(48,878) /gb=NM_004375 /gi=17921983 /ug=Hs.241515 /len=2717	NM_004375	Hs.241515	NP_004366
11337	0.020126	dihydropyrimidine dehydrogenase (DPYD), mRNA /cds=(102,3179) /gb=NM_000110 /gi=4557874 /ug=Hs.1602 /len=4407	NM_000110	Hs.1602	NP_000101
11338	0.011228	Similar to SRY-box containing gene 5, clone IMAGE:3919439, mRNA /gb=BC014929 /gi=15928923 /ug=Hs.383009 /len=652	BC014929	Hs.383009	
11349	0.022485	hypothetical nuclear factor SBBI22 (LOC57117), mRNA /cds=(207,1595) /gb=NM_020395 /gi=21361850 /ug=Hs.432952 /len=1716	NM_020395	Hs.432952	NP_065128
11369	0.04638	clone IMAGE:5301545, mRNA /gb=BC041951 /gi=27469737 /ug=Hs.177781 /len=2155	BC041951	Hs.177781	
11371	0.01798	FLJ13700 fis, clone PLACE2000216, highly similar to SPECTRIN BETA CHAIN, BRAIN /cds=UNKNOWN /gb=AK023762 /gi=10435792 /ug=Hs.324648 /len=3334	AK023762	Hs.324648	NP_842565
11374	0.014265	peptidyl-prolyl isomerase G (cyclophilin G) (PPIG), mRNA /cds=(158,2422) /gb=NM_004792 /gi=4758105 /ug=Hs.77965 /len=2695	NM_004792	Hs.77965	NP_004783
11394	0.016031	hypothetical protein CL25022 (CL25022), mRNA /cds=(158,1048) /gb=NM_015702 /gi=7661547 /ug=Hs.5324 /len=1416	NM_015702	Hs.5324	NP_056517
11404	0.038054	hypothetical protein MGC3067 (MGC3067), mRNA /cds=(140,895) /gb=NM_024295 /gi=13236515 /ug=Hs.323114 /len=1203	NM_024295	Hs.323114	NP_077271

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11411	0.034378	DKFZP434D1335 protein (DKFZP434D1335), mRNA /cds=(78,1469) /gb=NM_015578 /gi=24308092 /ug=Hs.8258 /len=3389	NM_015578	Hs.8258	NP_056393
11433	0.01798	annexin A7 (ANXA7), transcript variant 2, mRNA /cds=(61,1527) /gb=NM_004034 /gi=4809278 /ug=Hs.386741 /len=2176	NM_004034	Hs.386741	NP_004025
11444	0.034378	coproporphyrinogen oxidase (coproporphyrin, harderoporphyrin) (CPO), mRNA /cds=(68,1432) /gb=NM_000097 /gi=20127405 /ug=Hs.89866 /len=2691	NM_000097	Hs.89866	NP_000088
11446	0.04638	ornithine decarboxylase antizyme 1 (OAZ1), mRNA /gb=NM_004152 /gi=9845504 /ug=Hs.281960 /len=986	NM_004152	Hs.281960	NP_004143
11472	0.012669	similar to RIKEN cDNA 1110018M03, clone MGC:24932 IMAGE:4938507, mRNA, complete cds /cds=(218,853) /gb=BC026873 /gi=20073062 /ug=Hs.32478 /len=1826	BC026873	Hs.32478	
11473	0.04638	hypothetical protein BC013035 (LOC114926), mRNA /cds=(128,430) /gb=NM_138436 /gi=19923964 /ug=Hs.10018 /len=836	NM_138436	Hs.10018	NP_612445
11476	0.009931	clone IMAGE:3866125, mRNA /gb=BC035467 /gi=22028050 /ug=Hs.301226 /len=2297	BC035467	Hs.301226	
11480	0.031002	hypothetical protein FLJ23751 (FLJ23751), mRNA /cds=(121,1563) /gb=NM_152282 /gi=22748648 /ug=Hs.37443 /len=2994	NM_152282	Hs.37443	NP_689495
11481	0.042048	eps8 binding protein e3B1 mRNA, complete cds	AF006516		NP_005461
11482	0.04638	clone IMAGE:5271722, mRNA /gb=BC038786 /gi=24270905 /ug=Hs.190456 /len=1535	BC038786	Hs.190456	
11484	0.034378	casein alpha s1 (CSN1S1), mRNA /cds=(50,607) /gb=NM_001890 /gi=4503084 /ug=Hs.3155 /len=981	NM_001890	Hs.3155	NP_001881
11497	0.034378	FK506 binding protein 14, 22 kDa (FKBP14), mRNA /cds=(146,781) /gb=NM_017946 /gi=8923658 /ug=Hs.264636 /len=2248	NM_017946	Hs.264636	NP_060416
11505	0.027906	creatine kinase, brain (Ckb), mRNA	NM_021273		NP_067248
11513	0.020126	sulfatase SULF1 precursor, mRNA, complete cds /cds=(707,3322) /gb=AF545571 /gi=28191289 /ug=Hs.70823 /len=5699	AF545571	Hs.70823	NP_055985

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11516	0.01798	602943821F1 NIH_MGC_19 cDNA clone IMAGE:5091917 5', mRNA sequence /clone=IMAGE:5091917 /clone_end=5' /gb=BI194863 /gi=14649883 /ug=Hs.444288 /len=863	BI194863	Hs.444288	
11517	0.002982	fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA	NM_005103		NP_072043
11518	0.025072	RAB22A, member RAS oncogene family (RAB22A), mRNA /cds=(241,825) /gb=NM_020673 /gi=10190713 /ug=Hs.288968 /len=1728	NM_020673	Hs.288968	NP_065724
11520	0.022485	MYLE protein (MYLE), mRNA /cds=(12,299) /gb=NM_014015 /gi=13384596 /ug=Hs.11902 /len=1120	NM_014015	Hs.11902	NP_054734
11536	0.04638	EST(yh89e10.r1 cDNA clone 136938 5') 8e-06 match	R38461		NP_001002
11570	0.020126	clone IMAGE:5295896, mRNA /gb=BC043240 /gi=27695834 /ug=Hs.104413 /len=2136	BC043240	Hs.104413	
11587	0.034378	EST(qa18c02.x1 NCI_CGAP_Brn23 clone IMAGE:1687106 3' gb:M62762 VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT)	AI094920		NP_001685
11588	0.020126	EST(oz13e06.x1 Soares_fetal_liver_spleen_1NFLS_S1 clone IMAGE:1675234 3')	AI078464		
11590	0.038054	UI-E-EJ0-aig-j-08-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-aig-j-08-0-UI 3', mRNA sequence /clone=UI-E-EJ0-aig-j-08-0-UI /clone_end=3' /gb=BM682503 /gi=18992399 /ug=Hs.446242 /len=1052	BM682503	Hs.446242	
11597	0.020126	EST HUM517A08B Clontech human placenta polyA mRNA (#6572) Human sapiens cDNA clone GEN-517A08 5'	D63277		
11612	0.034378	Tho2 mRNA, complete cds /cds=(1,4437) /gb=AF441770 /gi=20799317 /ug=Hs.16411 /len=4452	AF441770	Hs.16411	
11657	0.04638	hypothetical protein FLJ23320 (FLJ23320), mRNA /cds=(117,2195) /gb=NM_024672 /gi=13375933 /ug=Hs.85910 /len=2337	NM_024672	Hs.85910	NP_078948

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11701	0.042048	of yeast long chain polyunsaturated fatty acid elongation enzyme 2 (HELO1), mRNA /cds=(345,1244) /gb=NM_021814 /gi=21361903 /ug=Hs.250175 /len=3011	NM_021814	Hs.250175	NP_068586
11702	0.04638	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA /cds=(63,1451) /gb=NM_001402 /gi=25453469 /ug=Hs.422118 /len=1837	NM_001402	Hs.422118	NP_001393
11703	0.016031	hypothetical protein MGC3295 (MGC3295), mRNA /cds=(510,1748) /gb=NM_025246 /gi=13376859 /ug=Hs.101257 /len=1958	NM_025246	Hs.101257	NP_079522
11704	0.014265	solute carrier family 1 (neutral amino acid transporter), member 5 (SLC1A5), mRNA /cds=(591,2216) /gb=NM_005628 /gi=5032092 /ug=Hs.183556 /len=2856	NM_005628	Hs.183556	NP_005619
11707	0.020126	transmembrane 4 superfamily member 2 (TM4SF2), mRNA /cds=(62,811) /gb=NM_004615 /gi=21265103 /ug=Hs.82749 /len=1813	NM_004615	Hs.82749	NP_004606
11767	0.04638	Purkinje cell protein 4 (PCP4), mRNA /cds=(58,246) /gb=NM_006198 /gi=5453857 /ug=Hs.80296 /len=540	NM_006198	Hs.80296	NP_006189
11774	0.027906	FLJ30424 fis, clone BRACE2008881, weakly similar to ZINC FINGER PROTEIN 195 /cds=UNKNOWN /gb=AK054986 /gi=16549625 /ug=Hs.21423 /len=2144	AK054986	Hs.21423	
11775	0.011228	UI-E-CQ1-acq-f-05-0-UI.r1 UI-E-CQ1 cDNA clone UI-E-CQ1-acq-f-05-0-UI 5', mRNA sequence /clone=UI-E-CQ1-acq-f-05-0-UI /clone_end=5' /gb=BM688680 /gi=19001938 /ug=Hs.406520 /len=934	BM688680	Hs.406520	
11780	0.014265	mRNA for KIAA1559 protein, partial cds. /cds=(61,1695) /gb=AB046779 /gi=10047182 /ug=Hs.35524 /len=5659	AB046779	Hs.35524	
11787	0.022485	inhibitor of Bruton's tyrosine kinase (IBTK), mRNA /cds=(420,1031) /gb=NM_015525 /gi=24308082 /ug=Hs.306425 /len=2240	NM_015525	Hs.306425	NP_056340
11810	0.016031	egl nine 3 (C. elegans) (EGLN3), mRNA /cds=(327,1046) /gb=NM_022073 /gi=11545786 /ug=Hs.18878 /len=2770	NM_022073	Hs.18878	NP_203130

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11818	0.04638	clone 23698 mRNA sequence /gb=AF052094 /gi=3360400 /ug=Hs.8136 /len=1264	AF052094	Hs.8136	
11822	0.038054	protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C), mRNA /cds=(89,1633) /gb=NM_002719 /gi=4506022 /ug=Hs.171734 /len=4064	NM_002719	Hs.171734	NP_848703
11840	0.04638	mitogen-activated protein kinase kinase 2 (MAP3K2), mRNA /cds=(102,1964) /gb=NM_006609 /gi=21735555 /ug=Hs.28827 /len=3336	NM_006609	Hs.28827	NP_006600
11843	0.012669	kinesin family member 13B (KIF13B), mRNA /cds=(38,5518) /gb=NM_015254 /gi=13194196 /ug=Hs.15711 /len=8743	NM_015254	Hs.15711	NP_056069
11859	0.027906	hypothetical protein FLJ13590 (FLJ13590), mRNA /cds=(465,2210) /gb=NM_024840 /gi=21362002 /ug=Hs.183390 /len=2225	NM_024840	Hs.183390	NP_079116
11922	0.025072	Hypothetical protein MGC30022, cDNA FLJ12832 fis, clone NT2RP2003137 /cds=UNKNOWN /gb=AK022894 /gi=10434551 /ug=Hs.179852 /len=2540	AK022894	Hs.179852	NP_689490
11927	0.031002	CCR4-NOT transcription complex, subunit 8 (CNOT8), mRNA /cds=(245,1123) /gb=NM_004779 /gi=24496777 /ug=Hs.26703 /len=2489	NM_004779	Hs.26703	NP_004770
11932	0.034378	LIN-7 protein 3, cDNA: FLJ21887 fis, clone HEP03135, highly similar to AF090900 Homo sapiens clone HQ0189 PRO0189 mRNA /cds=UNKNOWN /gb=AK025540 /gi=10438087 /ug=Hs.91393 /len=2440	AK025540	Hs.91393	NP_060832
11947	0.042048	polymerase (RNA) II (DNA directed) polypeptide H (POLR2H), mRNA /cds=(88,540) /gb=NM_006232 /gi=14589952 /ug=Hs.432574 /len=821	NM_006232	Hs.432574	NP_006223
11962	0.038054	aquaporin 3 (AQP3), mRNA /cds=(63,941) /gb=NM_004925 /gi=22165421 /ug=Hs.234642 /len=1835	NM_004925	Hs.234642	NP_004916

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
11968	0.025072	likely ortholog of mouse Mak3p (S. cerevisiae) (MAK3P), mRNA /cds=(301,810) /gb=NM_025146 /gi=13376734 /ug=Hs.288932 /len=3576	NM_025146	Hs.288932	NP_079422
12005	0.04638	EST(no44e03.s1 NCI_CGAP_Pr23 cDNA clone IMAGE:1103548)	AA622352		
12064	0.012669	oq82d05.x5 NCI_CGAP_Kid6 cDNA clone IMAGE:1592841 3', mRNA sequence /clone=IMAGE:1592841 /clone_end=3' /gb=AI733421 /gi=5054534 /ug=Hs.337206 /len=508	AI733421	Hs.337206	
12067	0.012669	UI-H-ED1-axq-o-07-0-UI.s1 NCI_CGAP_ED1 cDNA clone UI-H-ED1-axq-o-07-0-UI 3', mRNA sequence /clone=UI-H-ED1-axq-o-07-0-UI /clone_end=3' /gb=CA445564 /gi=24809984 /ug=Hs.243319 /len=539	CA445564	Hs.243319	
12077	0.034378	QV0-LT0015-180200-127-c04 LT0015)	AW835461		NP_006241
12147	0.020126	cDNA sequence(cDNA sequence DKFZp586J101 (from clone cDNA sequence DKFZp586J101))	AL050376		
12176	0.038054	engulfment and cell motility 2 (ced-12 C. elegans) (ELMO2), transcript variant 1, mRNA /cds=(141,2303) /gb=NM_133171 /gi=19718768 /ug=Hs.96560 /len=3630	NM_133171	Hs.96560	NP_573403
12187	0.031002	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax Drosophila) (MLL5), mRNA /cds=(202,5778) /gb=NM_018682 /gi=23503326 /ug=Hs.333300 /len=6543	NM_018682	Hs.333300	NP_061152
12190	0.011228	oxysterol binding protein-like 11 (OSBPL11), mRNA /cds=(306,2549) /gb=NM_022776 /gi=23111058 /ug=Hs.61260 /len=4206	NM_022776	Hs.61260	NP_073613
12201	0.012669	EST (Soares placenta Nb2HP IMAGE:143740 3')	R76686		
12202	0.034378	F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA /cds=(298,1584) /gb=NM_012158 /gi=16306583 /ug=Hs.7540 /len=3489	NM_012158	Hs.7540	NP_036290
12231	0.042048	EST (UI-H-BI3-akf-b-05-0-UI.s1 NCI_CGAP_Sub5 clone IMAGE:2734017 3')	AW449060		NP_061174
12233	0.042048	chemokine-like factor super family 3 (CKLFSF3), mRNA /cds=(527,1075) /gb=NM_144601 /gi=21389400 /ug=Hs.7773 /len=2318	NM_144601	Hs.7773	NP_653202



TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12237	0.016031	EST (602496405F1 NIH_MGC_75 clone IMAGE:4610376 5')	BG433151		
12238	0.020126	hypothetical protein LOC115286 (LOC115286), mRNA /cds=(189,740) /gb=NM_173471 /gi=27735034 /ug=Hs.379386 /len=1873	NM_173471	Hs.379386	NP_775742
12249	0.041895	7q24c01.x1 NCI_CGAP_GC6 cDNA clone IMAGE:3699073 3', mRNA sequence /clone=IMAGE:3699073 /clone_end=3' /gb=BF222857 /gi=11130034 /ug=Hs.331205 /len=503	BF222857	Hs.331205	
12262	0.031002	EST (IL3-ET0114-281000-318-C11 ET0114)	BF870398		NP_037364
12264	0.04638	clone IMAGE:3909104, mRNA /gb=BC015719 /gi=16041698 /ug=Hs.8852 /len=3169	BC015719	Hs.8852	
12266	0.022485	DC2 protein (DC2), mRNA /cds=(60,509) /gb=NM_021227 /gi=24308270 /ug=Hs.103180 /len=1090	NM_021227	Hs.103180	NP_067050
12268	0.027906	EST (ys15b03.r1 Soares fetal liver spleen IMAGE:214829 5')	H74096		
12275	0.027906	EST(601885028F1 NIH_MGC_57 cDNA clone IMAGE:4103479 5')	BF218874		NP_003109
12294	0.034378	EST(7e58a12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3286654 3')	BE644843		NP_006845
12301	0.027906	UI-H-EZ1-bbc-h-11-0-UI.s1 NCI_CGAP_Ch2 cDNA clone UI-H-EZ1-bbc-h-11-0-UI 3', mRNA sequence /clone=UI-H-EZ1-bbc-h-11-0-UI /clone_end=3' /gb=BQ574842 /gi=21478159 /ug=Hs.235026 /len=1065	BQ574842	Hs.235026	
12309	0.020126	junctional adhesion molecule 3 (JAM3), mRNA /cds=(25,1092) /gb=NM_032801 /gi=21704285 /ug=Hs.334703 /len=3675	NM_032801	Hs.334703	NP_116190
12327	0.022485	wr27c02.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2488898 3' similar to WP:F31E8.2 CE02711 SNT-1: SYNAPTOTAGMIN ;, mRNA sequence /clone=IMAGE:2488898 /clone_end=3' /gb=AI971263 /gi=5768089 /ug=Hs.166959 /len=747	AI971263	Hs.166959	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12339	0.029136	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant) (COL3A1), mRNA /cds=(118,4518) /gb=NM_000090 /gi=15149480 /ug=Hs.119571 /len=5489	NM_000090	Hs.119571	NP_000081
12345	0.04638	ESTs, cDNA, 3' end /clone=IMAGE:4141713 /clone_end=3' /gb=BG236123 /gi=12749970 /ug=Hs.127325 /len=489	BG236123	Hs.127325	NP_009173
12370	0.022485	mRNA; cDNA DKFZp586N2424 (from clone DKFZp586N2424) /gb=AL157503 /gi=7018553 /ug=Hs.27552 /len=2220	AL157503	Hs.27552	
12384	0.012669	FLJ31039 fis, clone HSYRA2000221 /cds=UNKNOWN /gb=AK055601 /gi=16550371 /ug=Hs.311977 /len=2770	AK055601	Hs.311977	
12404	0.035996	clone IMAGE:5301545, mRNA /gb=BC041951 /gi=27469737 /ug=Hs.177781 /len=2155	BC041951	Hs.177781	
12408	0.048742	cDNA MR1-FN0010-290700-007-g10 FN0010 (=AC099562.1  Homo sapiens chromosome 1 clone RP11-213P13, WORKING DRAFT SEQUENCE, 3 unordered pieces)	BE834948		NP_803133
12413	0.020126	cDNA FLJ14244 fis, clone OVARC1000802. /gb=AK024306 /gi=10436654 /ug=Hs.397378 /len=1889	AK024306	Hs.397378	
12418	0.048742	yw19d08.r1 Morton Fetal Cochlea cDNA clone IMAGE:252687 5', mRNA sequence /clone=IMAGE:252687 /clone_end=5' /gb=H87947 /gi=1069526 /ug=Hs.188912 /len=411	H87947	Hs.188912	
12438	0.016598	AV686223 GKC cDNA clone GKCGXH11 5', mRNA sequence /clone=GKCGXH11 /clone_end=5' /gb=AV686223 /gi=10288086 /ug=Hs.221642 /len=916	AV686223	Hs.221642	
12473	0.042048	xc09d01.x1 NCI_CGAP_Co21 cDNA clone IMAGE:2583745 3' similar to contains MER14.t2 MER14 repetitive element ;, mRNA sequence /clone=IMAGE:2583745 /clone_end=3' /gb=AW083503 /gi=6038579 /ug=Hs.311987 /len=510	AW083503	Hs.311987	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12519	0.04638	EST(cDNA clone IMAGE:1637714 3' similar to contains Alu repetitive element;contains L1.t1 L1 repetitive element ;)	AI000800		
12550	0.025072	clone IMAGE:5019705, mRNA /gb=BC021287 /gi=18204277 /ug=Hs.184544 /len=2121	BC021287	Hs.184544	
12555	0.022485	ESTs, cDNA, 5' end /clone=IMAGE:4802969 /clone_end=5' /gb=BG698090 /gi=13965026 /ug=Hs.12876 /len=985	BG698090	Hs.12876	
12580	0.022485	No significant match	SEQ.ID.No.34		
12581	0.048742	no significant match, ORF+3(108~209)	SEQ.ID.No.40		
12582	0.016031	No significant match	SEQ.ID.No.47		
12644	0.005206	EST (RC0-HT0297-301099-011-a06 HT0297)	BE151529		
12647	0.034378	EST(tm39b03.x1 NCI_CGAP_Kid11 clone IMAGE:2160461 3' contains L1.b3 L1 repeat)	AI478484		
12668	0.042048	hypothetical protein FLJ13110 (FLJ13110), mRNA /cds=(145,750) /gb=NM_022912 /gi=12597656 /ug=Hs.7358 /len=3856	NM_022912	Hs.7358	NP_075063
12669	0.016031	hypothetical protein FLJ31438 (FLJ31438), mRNA /cds=(347,2107) /gb=NM_152385 /gi=22748824 /ug=Hs.24423 /len=2266	NM_152385	Hs.24423	NP_689598
12677	0.018649	hypothetical protein MGC12981 (MGC12981), mRNA /cds=(225,767) /gb=NM_032357 /gi=21362049 /ug=Hs.104203 /len=1644	NM_032357	Hs.104203	NP_115733
12687	0.031002	wr41b04.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2490223 3', mRNA sequence /clone=IMAGE:2490223 /clone_end=3' /gb=AI972618 /gi=5769444 /ug=Hs.370369 /len=225	AI972618	Hs.370369	
12711	0.005206	EST(ne80b06.s1 NCI_CGAP_Ew1 cDNA clone IMAGE:910547)	AA491607		
12712	0.025072	EST(xg51d02.x1 NCI_CGAP_Ut4 cDNA clone IMAGE:2631843 3' similar to contains Alu repetitive element)	AW150422		
12721	0.031002	EST (wg23f05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:2365953 3'	AI740626		

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12762	0.022485	wd19h11.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2328645 3', mRNA sequence /clone=IMAGE:2328645 /clone_end=3' /gb=AI674745 /gi=4875225 /ug=Hs.377373 /len=347	AI674745	Hs.377373	
12767	0.025072	EST (602326911F1 NIH_MGC_91 IMAGE:4428291 5')	BG036175		
12782	0.025072	EST (CM3-LT0042-271299-060-c05 LT0042 cDNA)	AW837690		
12822	0.034378	yu41a04.y5 Soares ovary tumor NbHOT cDNA clone IMAGE:236334 5' similar to contains Alu repetitive element, mRNA sequence /clone=IMAGE:236334 /clone_end=5' /gb=AI820819 /gi=5439898 /ug=Hs.193116 /len=567	AI820819	Hs.193116	
12824	0.004545	ubiquitin-conjugating enzyme E2G 1 (UBC7 C. elegans) (UBE2G1), mRNA /cds=(167,679) /gb=NM_003342 /gi=21314607 /ug=Hs.78563 /len=2430	NM_003342	Hs.78563	NP_003333
12855	0.01798	UI-E-EJ0-aik-i-20-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-aik-i-20-0-UI 5', mRNA sequence /clone=UI-E-EJ0-aik-i-20-0-UI /clone_end=5' /gb=BM727413 /gi=19048746 /ug=Hs.112619 /len=1667	BM727413	Hs.112619	
12861	0.034378	cDNA FLJ25876 fis, clone CBR02529. /gb=AK098742 /gi=21758849 /ug=Hs.375841 /len=1877	AK098742	Hs.375841	
12875	0.038054	clone FLB3344 PRO0845 mRNA, complete cds /gb=AF130048 /gi=11493402 /ug=Hs.6390 /len=2171	AF130048	Hs.6390	
12881	0.016031	UI-E-CK1-abp-g-01-0-UI.s1 UI-E-CK1 cDNA clone UI-E-CK1-abp-g-01-0-UI 3', mRNA sequence /clone=UI-E-CK1-abp-g-01-0-UI /clone_end=3' /gb=BM661590 /gi=18965457 /ug=Hs.229338 /len=1447	BM661590	Hs.229338	
12957	0.025072	xj85e09.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2664040 3', mRNA sequence /clone=IMAGE:2664040 /clone_end=3' /gb=AW173284 /gi=6439232 /ug=Hs.370871 /len=548	AW173284	Hs.370871	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
12965	0.014265	UI-H-ED1-axy-n-13-0-UI.s1 NCI_CGAP_ED1 cDNA clone IMAGE:5835468 3', mRNA sequence /clone=IMAGE:5835468 /clone_end=3' /gb=BQ009853 /gi=19734754 /ug=Hs.438790 /len=1069	BQ009853	Hs.438790	
13003	0.038054	BX108813 Soares retina N2b4HR cDNA clone IMAGp998E03436, mRNA sequence /clone=IMAGp998E03436_; IMAGE:22 0010 /gb=BX108813 /gi=27877460 /ug=Hs.144186 /len=668	BX108813	Hs.144186	
13040	0.008765	UI-E-EJ1-aji-d-10-0-UI.s1 UI-E-EJ1 cDNA clone UI-E-EJ1-aji-d-10-0-UI 3', mRNA sequence /clone=UI-E-EJ1-aji-d- 10-0-UI /clone_end=3' /gb=BM684333 /gi=18994229 /ug=Hs.17910 /len=1036	BM684333	Hs.17910	
13047	0.038054	novel	SEQ.ID.No.30		
13069	0.031002	EST(PM1-HT0422-160300-009-a12 HT0422 Homo sapiens cDNA, MRNA sequence)	BE160886		
13076	0.014265	UI-H-BI1-abw-h-07-0-UI.s1 NCI_CGAP_Sub3 cDNA clone IMAGE:2713572 3', mRNA sequence /clone=IMAGE:2713572 /clone_end=3' /gb=AW138111 /gi=6142429 /ug=Hs.436560 /len=800	AW138111	Hs.436560	
13092	0.025072	No significant match, ORF-1(155~328)	SEQ.ID.No.81		
13139	0.027906	chromosome 1 open reading frame 8 (C1orf8), mRNA /cds=(251,1222) /gb=NM_004872 /gi=27545320 /ug=Hs.416495 /len=1709	NM_004872	Hs.416495	NP_004863
13170	0.011228	nucleolar protein family 6 (RNA- associated) (NOL6), transcript variant alpha, mRNA /cds=(61,3501) /gb=NM_022917 /gi=22212928 /ug=Hs.183253 /len=4854	NM_022917	Hs.183253	NP_631981
13197	0.032415	similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA /cds=(67,558) /gb=NM_022731 /gi=12232386 /ug=Hs.118064 /len=1811	NM_022731	Hs.118064	NP_073568
13212	0.026138	hypothetical protein FLJ20060 (FLJ20060), mRNA /cds=(72,2078) /gb=NM_017645 /gi=24431978 /ug=Hs.54617 /len=2884	NM_017645	Hs.54617	NP_060115

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13237	0.042048	KIAA0635 gene product (KIAA0635), mRNA /cds=(833,3373) /gb=NM_014645 /gi=7662215 /ug=Hs.185091 /len=5138	NM_014645	Hs.185091	NP_055460
13274	0.031002	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa (TAF7), mRNA /cds=(741,1790) /gb=NM_005642 /gi=14717406 /ug=Hs.155188 /len=2310	NM_005642	Hs.155188	NP_005633
13278	0.008765	601660815R1 NIH_MGC_72 cDNA clone IMAGE:3915843 3', mRNA sequence /clone=IMAGE:3915843 /clone_end=3' /gb=BE966810 /gi=11772610 /ug=Hs.336116 /len=730	BE966810	Hs.336116	
13283	0.02729	SEC24 related gene family, member D ( <i>S. cerevisiae</i> ) (SEC24D), mRNA /cds=(201,3299) /gb=NM_014822 /gi=7662658 /ug=Hs.19822 /len=3988	NM_014822	Hs.19822	NP_055637
13303	0.012669	xf50g03.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2621524 3' similar to contains element MER4 repetitive element ;, mRNA sequence /clone=IMAGE:2621524 /clone_end=3' /gb=AW130421 /gi=6132026 /ug=Hs.329722 /len=719	AW130421	Hs.329722	
13317	0.038054	Mannosidase, alpha, class 1A, member 1, cDNA: FLJ20935 fis, clone ADSE01534 (AK024588.1)	AK024588	Hs.25253	NP_005898
13335	0.031002	hypothetical protein FLJ12118 (FLJ12118), mRNA /cds=(24,1718) /gb=NM_024537 /gi=13375694 /ug=Hs.381043 /len=1843	NM_024537	Hs.381043	NP_078813
13336	0.031002	EST388184 MAGE resequences, MAGN cDNA, mRNA sequence /gb=AW976075 /gi=8167298 /ug=Hs.401959 /len=698	AW976075	Hs.401959	
13341	0.04638	leucine aminopeptidase 3 (LAP3), mRNA /cds=(187,1746) /gb=NM_015907 /gi=7705687 /ug=Hs.182579 /len=2147	NM_015907	Hs.182579	NP_056991
13347	0.042048	general transcription factor IIB (GTF2B), mRNA /cds=(39,989) /gb=NM_001514 /gi=13435384 /ug=Hs.258561 /len=1268	NM_001514	Hs.258561	NP_001505
13348	0.01798	hypothetical protein FLJ14153 (FLJ14153), mRNA /cds=(31,1428) /gb=NM_022736 /gi=12232392 /ug=Hs.7503 /len=2161	NM_022736	Hs.7503	NP_073573

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13354	0.016031	catenin, beta like 1 (CTNNBL1), mRNA /cds=(95,1786) /gb=NM_030877 /gi=18644733 /ug=Hs.178576 /len=1900	NM_030877	Hs.178576	NP_110517
13355	0.042048	mRNA; cDNA DKFZp313E1815 (from clone DKFZp313E1815) /gb=AL833098 /gi=21733689 /ug=Hs.125031 /len=1937	AL833098	Hs.125031	
13366	0.014265	hypothetical protein DKFZp434I1916 (DKFZp434I1916), mRNA /cds=(144,563) /gb=NM_032245 /gi=14149959 /ug=Hs.334641 /len=800	NM_032245	Hs.334641	NP_115621
13376	0.025072	hypothetical protein FLJ20276 (FLJ20276), mRNA /cds=(134,3388) /gb=NM_017738 /gi=8923250 /ug=Hs.270502 /len=4790	NM_017738	Hs.270502	NP_060208
13379	0.031002	patched related protein translocated in renal cancer (TRC8), mRNA /cds=(215,2209) /gb=NM_007218 /gi=21314653 /ug=Hs.28285 /len=2481	NM_007218	Hs.28285	NP_009149
13391	0.038054	chondroitin sulfate GalNAcT-2 (GALNAcT-2), mRNA /cds=(336,1964) /gb=NM_018590 /gi=24429591 /ug=Hs.180758 /len=3745	NM_018590	Hs.180758	NP_061060
13441	0.025072	hypothetical protein FLJ10769 (FLJ10769), mRNA /cds=(15,1187) /gb=NM_018210 /gi=8922653 /ug=Hs.8083 /len=2659	NM_018210	Hs.8083	NP_060680
13477	0.032415	cytoplasmic FMR1 interacting protein 1 (CYFIP1), mRNA /cds=(53,3814) /gb=NM_014608 /gi=24307968 /ug=Hs.77257 /len=4394	NM_014608	Hs.77257	NP_055423
13478	0.04638	EST(xd92a04.x1 Soares_NFL_T_GBC_S1 clone IMAGE:2605038 3')	AW117454		NP_073592
13483	0.031002	EST(oy85h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 clone IMAGE:1672661 3')	AI038280		
13485	0.01798	UI-H-FE1-bdt-o-02-0-UI.s1 NCI_CGAP_FE1 cDNA clone UI-H-FE1-bdt-o-02-0-UI 3', mRNA sequence /clone=UI-H-FE1-bdt-o-02-0-UI /clone_end=3' /gb=BU630228 /gi=23296993 /ug=Hs.402266 /len=703	BU630228	Hs.402266	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13486	0.04638	catenin (cadherin-associated protein), alpha-like 1 (CTNNAL1), mRNA /cds=(44,2248) /gb=NM_003798 /gi=4503128 /ug=Hs.58488 /len=2446	NM_003798	Hs.58488	NP_003789
13491	0.04638	hypothetical protein MGC33602 (MGC33602), mRNA /cds=(140,748) /gb=NM_152391 /gi=22748836 /ug=Hs.274415 /len=1790	NM_152391	Hs.274415	NP_689604
13514	0.027906	cDNA FLJ39478 fis, clone PROST2013605. /gb=AK096797 /gi=21756367 /ug=Hs.372680 /len=2507	AK096797	Hs.372680	
13516	0.025072	EST(qo47f09.x1 NCI_CGAP_Lu5 clone IMAGE:1911689 3')	AI268689		
13523	0.012669	UI-H-DI0-auw-o-12-0-UI.s1 NCI_CGAP_DI0 cDNA clone IMAGE:5875427 3', mRNA sequence /clone=IMAGE:5875427 /clone_end=3' /gb=BM997944 /gi=19722845 /ug=Hs.444026 /len=753	BM997944	Hs.444026	
13545	0.044138	yg03b02.s1 Soares infant brain 1NIB cDNA clone IMAGE:30959 3', mRNA sequence /clone=IMAGE:30959 /clone_end=3' /gb=R42618 /gi=817379 /ug=Hs.12700 /len=441	R42618	Hs.12700	
13550	0.038054	cDNA FLJ39435 fis, clone PROST2004727. /gb=AK096754 /gi=21756318 /ug=Hs.376116 /len=2450	AK096754	Hs.376116	
13558	0.022485	DKFZP564O0823 protein (DKFZP564O0823), mRNA /cds=(171,905) /gb=NM_015393 /gi=7661631 /ug=Hs.105460 /len=2155	NM_015393	Hs.105460	NP_056208
13560	0.031002	EST (tz36f03.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2290685 3')	AI783534		
13562	0.011228	AGENCOURT_6653840 NIH_MGC_116 cDNA clone IMAGE:5761286 5', mRNA sequence /clone=IMAGE:5761286 /clone_end=5' /gb=BM924828 /gi=19375207 /ug=Hs.181174 /len=1422	BM924828	Hs.181174	
13569	0.031002	EST (tu41c10.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2253618 3' similar to contains Alu repetitive element;)	AI686385		
13582	0.01798	mRNA; cDNA DKFZp586M1819 (from clone DKFZp586M1819) /cds=(1,795) /gb=AL834255 /gi=21739805 /ug=Hs.355753 /len=1723	AL834255	Hs.355753	NP_848934



**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13598	0.025072	PP3731 mRNA sequence /cds=(1443,1751) /gb=AF258562 /gi=10834669 /ug=Hs.352231 /len=1946	AF258562	Hs.352231	
13600	0.04638	Cdc42 guanine nucleotide exchange factor (GEF) 9 (ARHGEF9), mRNA /cds=(802,2352) /gb=NM_015185 /gi=7662107 /ug=Hs.54697 /len=5413	NM_015185	Hs.54697	NP_056000
13612	0.04638	poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA /cds=(89,1189) /gb=NM_005016 /gi=14141167 /ug=Hs.63525 /len=1362	NM_005016	Hs.63525	NP_114366
13618	0.027906	B-cell CLL/lymphoma 10 (BCL10), mRNA /cds=(706,1407) /gb=NM_003921 /gi=20336470 /ug=Hs.193516 /len=2809	NM_003921	Hs.193516	NP_003912
13634	0.009931	non-SMC (structural maintenance of chromosomes) element 1 protein (NSE1), mRNA /cds=(24,794) /gb=NM_145080 /gi=21489972 /ug=Hs.284295 /len=992	NM_145080	Hs.284295	NP_659547
13646	0.011228	FLJ13090 fis, clone NT2RP3002142 /cds=UNKNOWN /gb=AK023152 /gi=10434945 /ug=Hs.287955 /len=2182	AK023152	Hs.287955	
13659	0.027906	hypothetical protein (HSPC016), mRNA /cds=(39,233) /gb=NM_015933 /gi=7705430 /ug=Hs.397853 /len=384	NM_015933	Hs.397853	NP_057017
13662	0.008765	hypothetical protein FLJ14936 (FLJ14936), mRNA /cds=(187,1125) /gb=NM_032864 /gi=24762235 /ug=Hs.5301 /len=2613	NM_032864	Hs.5301	NP_116253
13665	0.004545	ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA /cds=(22,459) /gb=NM_003350 /gi=12025664 /ug=Hs.79300 /len=1535	NM_003350	Hs.79300	NP_003341
13680	0.009931	transforming, acidic coiled-coil containing protein 2 (TACC2), mRNA /cds=(87,3167) /gb=NM_006997 /gi=11119413 /ug=Hs.272023 /len=3686	NM_006997	Hs.272023	NP_008928
13690	0.044138	mRNA; cDNA DKFZp566G1424 (from clone DKFZp566G1424) /gb=AL122043 /gi=6093233 /ug=Hs.19221 /len=4410	AL122043	Hs.19221	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13691	0.006784	POP4 (processing of precursor , S. cerevisiae) (POP4), mRNA /cds=(26,688) /gb=NM_006627 /gi=5729985 /ug=Hs.421667 /len=1133	NM_006627	Hs.421667	NP_006618
13700	0.014265	DJ467N11.1 protein, FLJ13127 fis, clone NT2RP3002911 /cds=UNKNOWN /gb=AK023189 /gi=10435003 /ug=Hs.143917 /len=3073	AK023189	Hs.143917	NP_071374
13709	0.04638	hypothetical protein MGC2560 (MGC2560), mRNA /cds=(195,551) /gb=NM_031452 /gi=13899288 /ug=Hs.80624 /len=1229	NM_031452	Hs.80624	NP_113640
13718	0.029136	hypothetical protein MGC5370 (MGC5370), mRNA /cds=(189,269) /gb=NM_032739 /gi=14249363 /ug=Hs.332938 /len=974	NM_032739	Hs.332938	NP_116128
13722	0.044138	cDNA FLJ13032 fis, clone NT2RP3001120, moderately similar to ZINC FINGER PROTEIN 136. /cds=(120,1730) /gb=AK023094 /gi=10434855 /ug=Hs.110956 /len=2316	AK023094	Hs.110956	
13731	0.025072	diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA /cds=(777,1670) /gb=NM_032564 /gi=14211870 /ug=Hs.334305 /len=2713	NM_032564	Hs.334305	NP_115953
13761	0.016031	optic atrophy 1 (autosomal dominant) (OPA1), nuclear gene encoding mitochondrial protein, transcript variant 8, mRNA /cds=(56,3103) /gb=NM_130837 /gi=18860844 /ug=Hs.147946 /len=6029	NM_130837	Hs.147946	NP_570850
13782	0.014265	citrate synthase (CS), nuclear gene encoding mitochondrial protein, mRNA /cds=(1,1401) /gb=NM_004077 /gi=4758075 /ug=Hs.239760 /len=1401	NM_004077	Hs.239760	NP_004068
13783	0.027906	centrin, EF-hand protein, 2 (CETN2), mRNA /cds=(48,566) /gb=NM_004344 /gi=4757901 /ug=Hs.82794 /len=1087	NM_004344	Hs.82794	NP_004335
13803	0.038054	Rho-related BTB domain containing 3 (RHOBTB3), mRNA /cds=(336,2171) /gb=NM_014899 /gi=7662355 /ug=Hs.10432 /len=4099	NM_014899	Hs.10432	NP_055714

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
13810	0.031002	hypothetical protein FLJ11577 (FLJ11577), mRNA /cds=(277,1182) /gb=NM_025159 /gi=13376758 /ug=Hs.289065 /len=1808	NM_025159	Hs.289065	NP_079435
13811	0.042048	hypothetical protein FLJ20360 (FLJ20360), mRNA /cds=(80,2305) /gb=NM_017782 /gi=8923334 /ug=Hs.26434 /len=3041	NM_017782	Hs.26434	NP_060252
13827	0.042048	proteasome (prosome, macropain) 26S subunit, ATPase, 1 (PSMC1), mRNA /cds=(49,1371) /gb=NM_002802 /gi=24430150 /ug=Hs.4745 /len=1586	NM_002802	Hs.4745	NP_002793
13860	0.04638	hypothetical protein DKFZp564F013 (DKFZP564F013), mRNA /cds=(107,2194) /gb=NM_020432 /gi=24308192 /ug=Hs.128653 /len=4572	NM_020432	Hs.128653	NP_065165
13878	0.034378	EST(yr18g03.r1 cDNA clone 205684 5')	H63006		
13914	0.022485	hypothetical protein FLJ11193 (FLJ11193), mRNA /cds=(115,1443) /gb=NM_018356 /gi=8922930 /ug=Hs.151046 /len=2719	NM_018356	Hs.151046	NP_060826
13932	0.038054	EST(zr99b03.r1 NCI_CGAP_GCB1 clone IMAGE:683789 5')	AA236732		NP_690869
13939	0.022485	EST(ys82e11.r1 clone 221324 5')	H92037		NP_803133
13953	0.04638	hypothetical protein FLJ20287 (FLJ20287), mRNA /cds=(132,2921) /gb=NM_017746 /gi=8923268 /ug=Hs.26369 /len=3043	NM_017746	Hs.26369	NP_060216
13954	0.020126	EST nw48e08.s1 NCI_CGAP_Ew1 IMAGE:1249862	AA730589		
13984	0.042048	to90d01.x1 NCI_CGAP_Gas4 cDNA clone IMAGE:2185537 3' similar to contains L1.t1 L1 repetitive element ;, mRNA sequence /clone=IMAGE:2185537 /clone_end=3' /gb=AI801509 /gi=5366981 /ug=Hs.436925 /len=446	AI801509	Hs.436925	
14015	0.022485	EST(AV713804 DCB cDNA clone DCBAXA05 5')	AV713804		NP_004853
14018	0.009931	EST (Soares_senescent_fibroblasts_NbHSF clone IMAGE:1682209 3')	AI086864		NP_002517

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14021	0.034378	UI-E-EJ0-ahg-j-09-0-UI.r1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahg-j-09-0-UI 5', mRNA sequence /clone=UI-E-EJ0-ahg-j-09-0-UI /clone_end=5' /gb=BM712784 /gi=19026042 /ug=Hs.278378 /len=1255	BM712784	Hs.278378	
14023	0.04638	cDNA sequence FLJ12285 fis, clone MAMMA1001764	AK022347		
14056	0.04638	mRNA for KIAA1748 protein, partial cds. /cds=(1120,3396) /gb=AB051535 /gi=12698040 /ug=Hs.27239 /len=4545	AB051535	Hs.27239	
14057	0.027906	cDNA FLJ90553 fis, clone OVARC1000853. /cds=(116,748) /gb=AK075034 /gi=22760867 /ug=Hs.406158 /len=1673	AK075034	Hs.406158	
14060	0.004545	beta-amyloid binding protein precursor (BBP), mRNA /cds=(304,927) /gb=NM_032027 /gi=17738309 /ug=Hs.333541 /len=1250	NM_032027	Hs.333541	NP_114416
14066	0.016031	cDNA sequence FLJ13663 fis, clone PLACE1011646, highly similar to H.sapiens clone	AK023725		NP_003817
14067	0.034378	EST (zh68h11.r1 Soares_fetal_liver_spleen_1NFLS_S1 clone IMAGE:417285 5')	W87789		
14085	0.034378	EST (np87f03.s1 NCI_CGAP_Thy1 IMAGE:1133309)	AA632677		
14087	0.042048	EST ab74g12.s1 Stratagene fetal retina 937202 H.sapiens cDNA clone IMAGE:852742 3'	AA668159		NP_054767
14097	0.04638	MR0-HT0559-290500-027-d10 HT0559 cDNA, mRNA sequence /gb=BE708268 /gi=10096533 /ug=Hs.209224 /len=619	BE708268	Hs.209224	
14100	0.00772	7n87e11.x1 NCI_CGAP_Ov18 cDNA clone IMAGE:3571677 3', mRNA sequence /clone=IMAGE:3571677 /clone_end=3' /gb=BF195714 /gi=11082893 /ug=Hs.439426 /len=458	BF195714	Hs.439426	
14109	0.013065	wq35e02.x1 NCI_CGAP_GC6 cDNA clone IMAGE:2473274 3', mRNA sequence /clone=IMAGE:2473274 /clone_end=3' /gb=AI950442 /gi=5742752 /ug=Hs.176956 /len=496	AI950442	Hs.176956	
14134	0.038054	EST (602302386F1 NIH_MGC_87 cDNA clone IMAGE:4403877 5')	BG034307		NP_001943
14144	0.006784	EST (AU143964 HEMBA1 cDNA clone HEMBA1000519 3')	AU143964		NP_057535

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14168	0.020126	7j81h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 cDNA clone IMAGE:3392889 3', mRNA sequence /clone=IMAGE:3392889 /clone_end=3' /gb=BF055560 /gi=10809456 /ug=Hs.298968 /len=506	BF055560	Hs.298968	
14173	0.044138	Wilms' tumour 1-associating protein (WTAP), transcript variant 1, mRNA /cds=(223,1413) /gb=NM_004906 /gi=23199972 /ug=Hs.119 /len=2143	NM_004906	Hs.119	NP_690597
14174	0.034378	mitochondrion, complete genome	NC_001807		
14178	0.042048	EST(cDNA PM4-EN0063-051100-003-g09 EN0063)	BF848451		
14200	0.011228	EST(wf59e08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2359910 3')	AI809898		
14201	0.011904	EST(te67a08.x1 Soares_NFL_T_GBC_S1 cDNA clone IMAGE:2091734 3')	AI377927		
14209	0.025072	BX109160 Soares_NhHMPu_S1 cDNA clone IMAGp998H024744, mRNA sequence /clone=IMAGp998H024744_/_IMAGE:1 933489 /gb=BX109160 /gi=27877586 /ug=Hs.308982 /len=483	BX109160	Hs.308982	
14235	0.025072	hypothetical protein MGC45400 (MGC45400), mRNA /cds=(245,598) /gb=NM_153333 /gi=23503246 /ug=Hs.389734 /len=1290	NM_153333	Hs.389734	NP_699164
14243	0.022485	cDNA FLJ36574 fis, clone TRACH2012376. /gb=AK093893 /gi=21752845 /ug=Hs.356595 /len=1952	AK093893	Hs.356595	
14250	0.027906	ferritin, light polypeptide (FTL), mRNA /cds=(189,716) /gb=NM_000146 /gi=20149497 /ug=Hs.430150 /len=878	NM_000146	Hs.430150	NP_000137
14272	0.04638	nuclear protein double minute 1 (MDM1), mRNA /cds=(93,2237) /gb=NM_017440 /gi=24586654 /ug=Hs.12871 /len=2942	NM_017440	Hs.12871	NP_064513
14279	0.01798	AL535026 LTI_FL013_FBrn1 cDNA clone CS0DF007YJ21 3 prime, mRNA sequence /clone=CS0DF007YJ21 /clone_end=3' /gb=AL535026 /gi=12798519 /ug=Hs.268474 /len=921	AL535026	Hs.268474	

**TABLE 3N**

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14284	0.027906	hypothetical protein FLJ23751 (FLJ23751), mRNA /cds=(121,1563) /gb=NM_152282 /gi=22748648 /ug=Hs.37443 /len=2994	NM_152282	Hs.37443	NP_689495
14288	0.034378	small acidic protein (SMAP), mRNA /cds=(137,688) /gb=NM_014267 /gi=20070245 /ug=Hs.78050 /len=1504	NM_014267	Hs.78050	NP_055082
14380	0.042048	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa (NDUFB1), mRNA /cds=(34,210) /gb=NM_004545 /gi=27597086 /ug=Hs.183435 /len=290	NM_004545	Hs.183435	NP_004536
14382	0.038054	mRNA; cDNA DKFZp434P1018 (from clone DKFZp434P1018); partial cds /cds=UNKNOWN /gb=AL137527 /gi=6808195 /ug=Hs.289038 /len=3327	AL137527	Hs.289038	NP_116162
14409	0.04638	ESTs, cDNA, 3' end /clone=IMAGE:384992 /clone_end=3' /gb=AA709133 /gi=2719051 /ug=Hs.180144 /len=428	AA709133	Hs.180144	
14425	0.00772	wc34a07.x1 NCI_CGAP_Pr28 cDNA clone IMAGE:2317044 3' similar to contains element MSR1 repetitive element ;, mRNA sequence /clone=IMAGE:2317044 /clone_end=3' /gb=AI745524 /gi=5113812 /ug=Hs.205153 /len=398	AI745524	Hs.205153	
14487	0.038054	Cloning vector pAS2, complete sequence	U30496		
14520	0.01798	cDNA FLJ90504 fis, clone NT2RP3004090, weakly similar to GOLIATH PROTEIN. /cds=(103,1305) /gb=AK074985 /gi=22760786 /ug=Hs.171802 /len=2452	AK074985	Hs.171802	NP_775918
14522	0.025072	EST(Soares fetal liver spleen	N72700		
14529	0.04638	hypothetical protein FLJ23033 (FLJ23033), mRNA /cds=(108,1826) /gb=NM_024686 /gi=13375957 /ug=Hs.96423 /len=2115	NM_024686	Hs.96423	NP_078962
14553	0.025072	hypothetical protein H41 (H41), mRNA /cds=(324,1100) /gb=NM_017548 /gi=24475997 /ug=Hs.283690 /len=3346	NM_017548	Hs.283690	NP_060018
14559	0.004596	EST hb88d08.x1 NCI_CGAP_Ut2 cDNA clone IMAGE:2890287 3'	AW439829		NP_620128

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14560	0.016031	TRAM-like protein (KIAA0057), mRNA /cds=(76,1188) /gb=NM_012288 /gi=6912449 /ug=Hs.153954 /len=6974	NM_012288	Hs.153954	NP_036420
14571	0.020912	EST(xx31a10.x1 NCI_CGAP_Ut1 clone IMAGE:2839098 3')	AW571469		NP_055260
14596	0.038054	AGENCOURT_8819408 NIH_MGC_18 cDNA clone IMAGE:6422878 5', mRNA sequence /clone=IMAGE:6422878 /clone_end=5' /gb=BQ941317 /gi=22356795 /ug=Hs.443078 /len=929	BQ941317	Hs.443078	
14618	0.005206	EST (UI-H-BI2-agh-g-08-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2724303 3')	AW291353		NP_061049
14623	0.042048	hypothetical protein FLJ35779 (FLJ35779), mRNA /cds=(42,1694) /gb=NM_152408 /gi=22748864 /ug=Hs.432726 /len=1698	NM_152408	Hs.432726	NP_689621
14631	0.027906	EST(12h2 retina cDNA randomly primed sublibrary)	W26795		
14642	0.038054	aa51h10.s1 NCI_CGAP_GCB1 cDNA clone IMAGE:824515 3' similar to contains MER30.b1 MER30 repetitive element ;, mRNA sequence /clone=IMAGE:824515 /clone_end=3' /gb=AA490540 /gi=2219713 /ug=Hs.336686 /len=378	AA490540	Hs.336686	
14650	0.04638	clone IMAGE:4139786, mRNA, partial cds /cds=(1,625) /gb=BC007901 /gi=14043927 /ug=Hs.433279 /len=1493	BC007901	Hs.433279	
14677	0.044138	cDNA, 5' end /clone=IMAGE:158873 /clone_end=5' /gb=R75776 /gi=850458 /ug=Hs.302485 /len=522	R75776	Hs.302485	NP_004356
14686	0.012669	chromosome 20 open reading frame 52 (C20orf52), mRNA /cds=(164,403) /gb=NM_080748 /gi=18152784 /ug=Hs.401703 /len=602	NM_080748	Hs.401703	NP_542786
14690	0.04638	cDNA FLJ35033 fis, clone OCBBF2016590, weakly similar to CELL SURFACE ANTIGEN 114/A10 PRECURSOR. /cds=(407,934) /gb=AK092352 /gi=21750925 /ug=Hs.156113 /len=2884	AK092352	Hs.156113	

TABLE 3N

Spot	p-value	Description	Gene Accession No.	Unigene Accession No.	Protein Accession No.
14777	0.038054	UI-E-EJ0-ahn-c-06-0-UI.s1 UI-E-EJ0 cDNA clone UI-E-EJ0-ahn-c-06-0-UI 3', mRNA sequence /clone=UI-E-EJ0-ahn-c-06-0-UI /clone_end=3' /gb=BM674956 /gi=18984854 /ug=Hs.131705 /len=1017	BM674956	Hs.131705	
14779	0.016031	UI-H-BI2-ahk-c-12-0-UI.s1 NCI_CGAP_Sub4 cDNA clone IMAGE:2727166 3', mRNA sequence /clone=IMAGE:2727166 /clone_end=3' /gb=AW294558 /gi=6701194 /ug=Hs.437134 /len=888	AW294558	Hs.437134	
14799	0.04638	DKFZp586J021 (from clone DKFZp586J021) /cds=UNKNOWN /gb=AL110197 /gi=5817115 /ug=Hs.6441 /len=1896	AL110197	Hs.6441	NP_003246
14804	0.014741	splicing factor, arginine/serine-rich 12 (SFRS12), mRNA /cds=(342,1868) /gb=NM_139168 /gi=21040254 /ug=Hs.381165 /len=3811	NM_139168	Hs.381165	NP_631907
14882	0.038054	DKFZp434C022_s1 434 (synonym: htes3) cDNA clone DKFZp434C022 3', mRNA sequence /clone=DKFZp434C022 /clone_end=3' /gb=AL044366 /gi=5432588 /ug=Hs.165805 /len=668	AL044366	Hs.165805	
14934	0.026138	No significant match (ORF:+1:1~102[102])	SEQ.ID.No.59		
14941	0.01798	brain cDNA clone:QmoA-10474, full insert sequence	AB062971		